

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.45573 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-11

Perfect score: 92
Sequence: 1 SGGTTVTVTLSDVNDNPP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	90.2	790	2	G02678 cadherin-14 - huma
2	83	90.2	793	2	D38992 cadherin 8 - huma
3	82	89.1	785	2	I50180 cadherin-7 - chick
4	81	88.0	790	2	I51638 F-cadherin - Afri
5	80	87.0	789	2	I52701 K-cadherin - rat
6	80	87.0	790	2	I50178 cadherin-6B - chic
7	80	87.0	790	2	I37016 cadherin-6 - huma
8	79	85.9	796	2	A38992 cadherin 11 precu
9	79	85.9	796	2	I48277 cadherin-11 - mous
10	79	85.9	796	2	I49556 cadherin-11 - mous
11	79	85.9	796	2	A53584 OB-cadherin precu
12	71	77.2	794	2	I59372 cadherin 12 - huma
13	67	72.8	780	2	T30213 G-cadherin - sea u
14	65	70.7	4351	2	T00252 MEGL1 protein - ra
15	62	67.4	784	1	IUHUC5 cadherin 5 precurs
16	62	67.4	877	1	IUBOCN N-cadherin 2 precurs
17	62	67.4	906	1	IUBOCN N-cadherin 2 precurs
18	62	67.4	906	1	IUMSCN N-cadherin precurs
19	62	67.4	912	1	IUCHCN N-cadherin precurs
20	61	66.3	913	1	A47543 R-cadherin precurs
21	61	66.3	913	1	IUCHCR R-cadherin precurs
22	61	66.3	2610	2	T20968 hypothetical prote
23	58	63.0	4307	2	T20721 hypothetical prote
24	57	62.0	713	2	B38992 cadherin 13 precu
25	57	62.0	770	2	B48810 desmocollin 1b pre
26	57	62.0	824	2	A48510 desmocollin 1a pre
27	57	62.0	840	2	I37281 Desclb precursor -
28	57	62.0	894	2	I37282 Desclb precursor -
29	57	62.0	905	1	IUXLC1 N-cadherin 1 precu

30	57	62.0	906	1	IUXLC2 N-cadherin 2 precu
31	57	62.0	1715	2	JR0128 Bombyx mori recept
32	57	62.0	3097	2	T00021 DN-cadherin - fnti
33	57	62.0	5147	1	IUFFTM cadherin-related t
34	56	60.9	373	2	T34563 hypothetical prote
35	56	60.9	882	1	IUHUCE cadherin 1 precurs
36	56	60.9	1069	2	T00043 BH-protocadherin-a
37	56	60.9	1072	2	T00041 BH-protocadherin P
38	56	60.9	1200	2	T00042 BH-protocadherin P
39	55	59.8	712	1	IUMSCT T-cadherin precurs
40	55	59.8	717	2	I51206 T-cadherin 2 - chi
41	55	59.8	896	2	I45858 desmocollin - bovl
42	55	59.8	3034	2	T14119 seven-pass transme
43	54	58.7	826	2	B53363 desmocollin, type
44	54	58.7	896	2	A53363 desmocollin, type
45	54	58.7	916	2	C38992 cadherin 4 precurs

ALIGNMENTS

RESULT 1

G02678
cadherin-14 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G02678
R/Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A/Reference number: H01584
A/Accession: G02678
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <SH1>
A/Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:G1389852; PIDN:AAH02933.1; PID:G13
C/Superfamily: cadherin; cadherin repeat homology <CDH>
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
DB 249 SGGTTVTVTLSDVNDNPP 266

RESULT 2

D38992
cadherin 8 - human
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MIMD:91283540; PMID:2059658
A/Accession: D38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-793 <SU2>
A/Cross-references: GB:I34060; NID:G506411; PIDN:AAA35628.1; PID:G506412
C/Genetics:
A/Genes: GDB:CDH8
A/Cross-references: GDB:5822911
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 793;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
|||:|||||
Db 250 SGGTTVTVTLSDVNDNPP 267

RESULT 3

I50180
C:Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I50180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: I50178; MUID:95309115; PMID:7540531
A/Accession: I50180
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-785 <NAK>
A/Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868004
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 89.1%; Score 82; DB 2; Length 785;
Best Local Similarity 83.3%; Pred. No. 7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
|||:|||||
Db 243 SGGTTVTVTLSDVNDNPP 260

RESULT 4

I51638
F-cadherin - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51638; S55391
R:Spesserth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A/Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A/Reference number: I51638; MUID:96039533; PMID:7496627
A/Accession: I51638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <ESP>
A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CA559679.1; PID:98546
C/Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 88.0%; Score 81; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 0.0001;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
|||:|||||
Db 248 AGTTTVTVTLSDVNDNPP 265

RESULT 5

I52701
K-cadherin - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: I52701
R:Xiang, Y. Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara,
Cancer Res. 54, 3034-3041, 1994
A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
A/Reference number: I52701; MUID:94243827; PMID:8187093
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-789 <RES>

A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:943546
C/Genetics:
A/Gene: KCAD
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 789;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
|||:|||||
Db 249 SGGTTVTVTLSDVNDNPP 266

RESULT 6

I50178
cadherin-6B - chicken
C/Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I50178
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe
A/Reference number: I50178; MUID:95309115; PMID:7540531
A/Accession: I50178
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <NAK>
A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA07720.1; PID:986799
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
|||:|||||
Db 249 SGGTTVTVTLSDVNDNPP 266

RESULT 7

I37016
cadherin-6 - human
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: I37016
R:Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the
A/Reference number: I37016; MUID:95262134; PMID:7743525
A/Accession: I37016
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:9974184; PIDN:BA06562.1; PID:997418
C/Genetics:
A/Gene: CDH6
A/Cross-references: GDB:5822908
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
|||:|||||
Db 249 SGGTTVTVTLSDVNDNPP 266

RESULT 8

A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jun-2004
C:Accession: A38992
R: Suzuki, S., Sano, K., Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A:Reference number: S24305; MUID:91283540; PMID:2059658
A:Accession: A38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <SUZ>
A:Cross-references: UNIPROT:P55287; GB:L34056; NID:G506403; PIDN:AAA3622.1; PID:G506404
C:Genetics:
A:Gene: GDB:CDH11; OB
A:Cross-references: GDB:512891; OMIM:600023
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:56-159/Domain: cadherin repeat homology <CR1>
F:163-268/Domain: cadherin repeat homology <CR2>
F:271-383/Domain: cadherin repeat homology <CR3>
F:386-468/Domain: cadherin repeat homology <CR4>

	Query Match	85.9%	Score 79;	DB 2;	Length 796;
	Similarity	77.8%	Pred. No.	0.00021;	
Bb	Best Local		Mismatches	1;	Gaps 0;
	Matches	14;	Conservative	3;	
Oy					
	1	GGSTTATVLTLDVNDNPP	18		
	SGTTKVVITLTDVNDNPP	266			

```

RESULT 9
148277
cadherin-11 - mouse
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: I48277
R.Hofmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A.Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A.Reference number: I48277; PMID:95269886; PMID:7750649
A.Accession: I48277

```

A:Accession: AF000001
 A:Molecular type: mRNA
 A:Residues: 1-796 <RES>
 A:Citostere-references: UNIPROT:P55288; EMBL:X77557; NID:G642796; PIDD:CAA54674.1; PIDD:G66600
 C:Gene: cad-11
 C:Superfamily: cadherin / cadherin repeat homology
 F:56-159/Domain: cadherin repeat homology <CDH>

	Query Match Similarity	85.9%	Score 79	DB 2	length 796
Best Local Similarity	77.8%	Pred No.	0	00021	
Matches	14	Conservative	3	Mismatches	1
				Indels	0
				Gaps	0
QY	1	SGSTTVTVTLTSDVNDNP	18		
		: : : : : :			
Db	249	SGSTKVTITLTLDVNDNP	266		

RESULT 10
 149556
 cadherin-11 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 149556
 R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
 Dev. Biol. 169, 347-358, 1995
 A:Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head

A,Reference number: I49556, MUID:95269887, PMID:7750650
A,Accession: I49556
A,Status: preliminary; translated from GB/EMBL/DBJ
A,Molecule type: mRNA
A,Residues: 1-796 <RES>
A,Cross-references: UNIPROT:P55288, GB:D31963, NID:G974190, PIDN:BAA06730.1, PID:G974199
C,Superfamily: cadherin; cadherin repeat homology
F56-159/Domain: cadherin repeat homology <CDH>

Query	1	SGSTTIVTSLDNDNP	18
	:		
DB	249	SGTIVTITLTDVNDNP	266
	:		
Matches	14	Conservative	3
		Mismatches	1
		Indels	0
		Gaps	0
Score	79	DB 2	Length 796
Best Local Similarity	77.8%	Pred. No.	0.00021

```

RESULT 11
A53584
O:cadherin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence (house mouse)
C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amann, E.
J. Biol. Chem. 269, 10592-12098, 1994
A>Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584; MUID:94216322; PMID:8165513
A:Accession: A53584
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D1253; NID:G994774; PIDN:BA04797.1; PID:G994777
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
F:56-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:386-488/Domain: cadherin repeat homology <CR4>

```

Query Match	85.9%	Score 79	DB 2	Length 796
Similarity	77.8%	Pred. No.	0.0021	
Best Local				
Matches	14	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0
QY	1	SGSTTYYTTLSDVNDNP	18	
		: : : : : : :		
Db	249	SGTTRITLLDNDNP	266	

RESULT 12
I59372
cadherin 12 - human
N:Alternate names: Br-cadherin
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence
C:Accession: I59372
R:Seelig, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.
Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
A>Title: Expressed cadherin pseudogenes are localized to the critical region of the spr
A:Reference number: I59372; KUID:95249541; PMID:773168
A:Accession: I59372
A>Status: nucleic acid sequence not shown; translated from GB/EN
A:Molecule type: mRNA
A:Features: 1-794 <ES>
A:Cross-references: UNIPROT:P55289; GB:L33477; NID:G793942; PIDD:AA84853.1; PID:G793942
C:Gene: GDB:CDH12
A:Cross-references: GDB:596324
A:Map position: 5p13-5p14
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; transmembrane protein
F:51-160/Domain: cadherin repeat homology <CR1>
F:163-269/Domain: cadherin repeat homology <CR2>
F:272-384/Domain: cadherin repeat homology <CR3>

F:387-489/Domain: cadherin repeat homology <CR4>
 F:491-601/Domain: cadherin repeat homology <CR5>
 F:610-637/Domain: transmembrane #status predicted <TM>
 F:638-794/Domain: intracellular #status predicted <INT>

Query Match 77.2%; Score 71; DB 2; Length 794;
 Best Local Similarity 66.7%; Pred. No. 0.0039;
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSVDVNDNP 18
 :|||:|||||
 Db 250 AGTTVTNLTLDVNDNP 267

RESULT 13

T30213
 G-cadherin - sea urchin (lytechinus variegatus)
 C:Species: lytechinus variegatus (variegated urchin)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30213
 R:Miller, J.R.; McClay, D.R.
 Dev. Biol. 192, 323-339, 1997
 A:Title: Characterization of the role of cadherin in regulating cell adhesion during sea
 A:Reference number: 220780; PMID:98104238; PMID:9441671
 A:Accession: T30213
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2809 <Full>
 A:Cross-references: UNIPROT:O61230; EMBL:U34823; NID:92982186; PID:92982187; PIDN:AA0063

Query Match 72.8%; Score 67; DB 2; Length 2809;
 Best Local Similarity 66.7%; Pred. No. 0.068;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSVDVNDNP 18
 :|||:|||||
 Db 1694 SGTATVATVTDVNDTP 1711

RESULT 14

T00252
 MEGF1 protein - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00252
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: 214126; PMID:98360089; PMID:9693030
 A:Accession: T00252
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4351 <NAK>
 A:Cross-references: UNIPROT:O88277; EMBL:AB011527; NID:93449285; PIDN:BAA32458.1; PID:G3

A:Experimental source: Brain
 C:Genetics:
 A:Gene: MEGF1
 C:Superfamily: rat MEGF1 protein; cadherin repeat homology; EGF homology; laminin G repe
 F:3758-3949/Domain: laminin G repeat homology <LGR>
 F:3953-3985/Domain: EGF homology <EGF>
 F:3992-4023/Domain: EGF homology <EGF>

Query Match 70.7%; Score 65; DB 2; Length 4351;
 Best Local Similarity 61.1%; Pred. No. 0.23;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSVDVNDNP 18
 :|||:|||||
 Db 2360 TGETLVVNVSDINDNP 2377

RESULT 15

ITRUCS

cadherin 5 precursor - human
 N:Alternate names: 7B4 antigen; cadherin, endothelial-specific; VE-cadherin
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: S49893; S24305; A43418
 R:Breviaro, F.; Cayula, L.; Corda, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lam
 submitted to the EMBL data library, June 1994
 A:Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a no
 A:Reference number: S49893
 A:Accession: S49893
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-784

A:Cross-references: UNIPROT:P33151; EMBL:X79981; NID:959833; PIDN:CAA5306.1; PID:G599
 R:Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous

A:Reference number: S24305; PMID:91283540; PMID:2059658
 A:Accession: S24305
 A:Molecule type: mRNA
 A:Residues: 5516; 'I', 518-784 <SUZ>
 A:Cross-references: EMBL:X59796; NID:9639976; PIDN:CAA42468.1; PID:929593
 R:Jampagnani, M.G.; Resnati, M.; Ralvert, M.; Pigott, R.; Pisacane, A.; Houen, G.; Ruco
 J. Cell Biol. 118, 1511-1522, 1992

A:Title: A novel endothelial-specific membrane protein is a marker of cell-cell contact
 A:Reference number: A43418; PMID:92394977; PMID:1522121
 A:Accession: A43418

A:Molecule type: protein
 A:Residues: 48-60; 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254
 A:Experimental source: cultured endothelial cells
 A:Note: sequence extracted from NCBI backbone (NCBI:113040, NCBI:113045, NCBI:113047
 C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
 C:Genetics:

A:Gene: GDB:CDH5

A:Cross-references: GDB:134230; OMIM:601120

A:Map position: 16q22.1-16q22.1
 C:Superfamily: cadherin; cadherin repeat homology
 C:Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-47/Domain: propeptide #status predicted <PRO>
 F:48-784/Domain: extracellular #status predicted <EXT>
 F:48-593/Domain: extracellular #status predicted <EXT>
 F:50-151/Domain: cadherin repeat homology <CR1>
 F:154-258/Domain: cadherin repeat homology <CR2>
 F:261-372/Domain: cadherin repeat homology <CR3>
 F:375-479/Domain: cadherin repeat homology <CR4>
 F:481-587/Domain: cadherin repeat homology <CR5>

F:594-620/Domain: transmembrane #status predicted <TM>
 F:621-784/Domain: intracellular #status predicted <INT>
 F:736-753/Region: serine-rich
 F:61,112,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 67.4%; Score 62; DB 1; Length 784;
 Best Local Similarity 66.7%; Pred. No. 0.1;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSVDVNDNP 18
 :|||:|||||
 Db 239 SGTATVATVTDVNDNP 256

Search completed: December 8, 2004, 10:27:07
 Job time : 1.45573 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 7.21488 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-11
Perfect score: 92
Sequence: 1 SGGTTVTTLSDVNDNPP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	370	2	Q86T00
2	92	100.0	493	2	Q96I07
3	92	100.0	781	2	Q6PFX6
4	92	100.0	781	2	AAH57373
5	92	100.0	819	1	CADO_HUMAN
6	83	90.2	337	2	Q8BIB5
7	83	90.2	508	2	Q6PAN4
8	83	90.2	508	2	AAH60200
9	83	90.2	716	2	Q8C375
10	83	90.2	716	2	Q8C449
11	83	90.2	716	2	AAH57581
12	83	90.2	754	2	Q8BRK4
13	83	90.2	790	1	CADI_HUMAN
14	83	90.2	799	1	CADH_HUMAN
15	83	90.2	799	1	CAD8_MOUSE
16	83	90.2	799	1	CAD8_RAT
17	82	89.1	340	2	Q8BIL4
18	82	89.1	551	2	Q8AMW2
19	82	89.1	630	2	Q8IY78
20	82	89.1	785	1	CAD7_CHICK
21	82	89.1	785	1	CAD7_HUMAN
22	82	89.1	785	1	Q8BWK2
23	81	88.0	790	2	Q91838
24	80	87.0	788	1	CADA_HUMAN
25	80	87.0	788	2	Q8OWS7
26	80	87.0	788	2	Q8VI68
27	80	87.0	788	2	AAH62962
28	80	87.0	789	1	CAD6_RAT
29	80	87.0	789	1	CADA_CHICK
30	80	87.0	790	1	CAD6_CHICK

32	80	87.0	790	1	CAD6_MOUSE	P97326 mus musculu
33	80	87.0	798	2	Q7ZYV7	Q7ZYV7 gallus gall
34	80	87.0	798	2	Q8QGH3	Q8QGH3 gallus gall
35	80	87.0	801	1	CADK_HUMAN	Q9BIB6 homo sapien
36	80	87.0	801	2	Q920M3	Q920M3 mus musculu
37	80	87.0	813	1	CADM_MOUSE	Q9WPD5 mus musculu
38	80	87.0	813	1	CADM_RAT	Q63115 ractus norv
39	80	87.0	828	1	CADM_HUMAN	Q9U199 homo sapien
40	79	85.9	792	1	CADB_CHICK	Q93119 gallus gall
41	79	85.9	794	2	Q93264	Q93264 xenopus lae
42	79	85.9	796	1	CAD8_HUMAN	P55287 homo sapien
43	79	85.9	796	1	CAD8_MOUSE	P55288 mus musculu
44	79	85.9	796	1	Q8C706	Q8C706 mus musculu
45	75	81.5	789	1	CAD9_HUMAN	Q9UBI4 homo sapien

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT;	370 AA.
ID	Q86T00	ID	Q86T00		
AC	Q86T00;	AC	Q86T00;		
DT	01-JUN-2003 (T-EMBLrel. 24, Created)	DT	01-JUN-2003 (T-EMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)	DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Full-length cDNA clone CS0DK003Y017 of Hela cells of Homo sapiens (human) (Fragment).	DE	Full-length cDNA clone CS0DK003Y017 of Hela cells of Homo sapiens (human) (Fragment).		
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
CX	NCBI_TaxID=9606;	CX	NCBI_TaxID=9606;		
LN	[1]	LN	[1]		
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.		
RC	TISSUE=Hela cells;	RC	TISSUE=Hela cells;		
RA	Li W.B., Gruber C., Jesse J., Polayes D.;	RA	Li W.B., Gruber C., Jesse J., Polayes D.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
RA	Genoscope;	RA	Genoscope;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Contains 4 cadherin domains.	CC	-1- SIMILARITY: Contains 4 cadherin domains.		
DR	EMBL; BX248303; CAD62630.1; -	DR	EMBL; BX248303; CAD62630.1; -		
DR	GO; GO:0005509; F:calcium ion binding; IEA.	DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.	DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.		
DR	InterPro; IPR002126; Cadherin.	DR	InterPro; IPR002126; Cadherin.		
DR	Pfam; PF000028; Cadherin; 3.	DR	Pfam; PF000028; Cadherin; 3.		
DR	PRINTS; PR00205; CADHERIN.	DR	PRINTS; PR00205; CADHERIN.		
DR	SMART; SM00112; CA; 2.	DR	SMART; SM00112; CA; 2.		
DR	PROSITE; PS00213; CADHERIN_1; 1.	DR	PROSITE; PS00213; CADHERIN_1; 1.		
DR	PROSITE; PS50268; CADHERIN_2; 4.	DR	PROSITE; PS50268; CADHERIN_2; 4.		
KW	Calcium; Calcium-binding.	KW	Calcium; Calcium-binding.		
FT	NON TER	FT	NON TER		
FT	NON TER	FT	NON TER		
SQ	SEQUENCE 370 AA; 39479 MW; 39964DAF8A450E0 CRC64;	SQ	SEQUENCE 370 AA; 39479 MW; 39964DAF8A450E0 CRC64;		
Query Match					
Best Local Similarity 100.0%; Score 92; DB 2; Length 370;					
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	SGS	TTVTTLSDVNDNPP	18	
DB	1	SGS	TTVTTLSDVNDNPP	18	
RESULT 2					
ID	Q96I07	ID	Q96I07		
AC	Q96I07;	AC	Q96I07;		
DT	01-DEC-2001 (T-EMBLrel. 19, Created)	DT	01-DEC-2001 (T-EMBLrel. 19, Created)		
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)	DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)		

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DS Hypothetical protein FLJ25193.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Nishikawa K., Wagatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsura N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Oseki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isogai T., Sugano S.,
 RC Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; AK057922; BAB71613.1; -
 DR HSSP; P12830; 1068.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016020; Cmembrane; IEA.
 DR GO; GO:0005509; Fcalcium ion binding; IEA.
 DR GO; GO:0007156; Fhomophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 4.
 DR Calcium; Calcium-binding.
 KW SEQUENCE 493 AA; 53618 MW; 33510DF63AF09C1E CRC64;
 SQ
 Query Match 100.0%; Score 92; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 6.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTVTVTLSVDVNDNP 18
 DB 240 SGSTVTVTLSVDVNDNP 257
 ID 06PFK6 PRELIMINARY; PRT; 781 AA.
 AC 06PFK6;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Ch24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsugu S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL; BC057373; AAH57373.1; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002333; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;
 SQ
 Query Match 100.0%; Score 92; DB 2; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTVTVTLSVDVNDNP 18
 DB 240 SGSTVTVTLSVDVNDNP 257
 ID AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373;
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN CDH24.
 GN Name=Ch24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ueda T.B., Toshitsugu S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC057373; AAH57373.1;
DR SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 100.0%; Score 92; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTTATLSDVNDNPP 18
DB 240 SGGTTTATLSDVNDNPP 257

RESULT 5
CADO_HUMAN STANDARD; PRT; 819 AA.
ID CADO_HUMAN Q9NT84;
AC Q86UP0; Q86UP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RA CATEININS.
RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA Kafetsios B.U., Nieman M.T., Wheelock M.J., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
RT II cadherin."
RL J. Biol. Chem. 278:27513-27519(2003).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Devel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Kilmowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seisagiri S., Simmons L., Singh U., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Weand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Testis;
RA Blum H., Baerach S., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
-1- They preferentially interact with themselves in a homophilic
-1- manner in connecting cells; cadherins may thus contribute to the
-1- sorting of heterogeneous cell types. Cadherin-24 mediate strong
-1- cell-cell adhesion.
-1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-1- ALTERNATIVE PRODUCTS:
-1- Event=Alternative splicing; Named isoforms=3;
-1- Name=1; Synonyms=long form;
-1- IsoId=Q86UP0-1; Sequence=Displayed;
-1- Name=2; Synonyms=short form;
-1- IsoId=Q86UP0-2; Sequence=VSP_008717;
-1- Name=3;
-1- Occurrence: 1
-1- Mus musculus (Mouse).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=1049636;
 RT Carninci P., Hayashizaki Y.;
 RL "High-efficiency full-length cDNA cloning";
 RM Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851;
 RT RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection";
 RM Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX The FANTOM Consortium;
 RT The RIKEN Genome Exploration Research Group Phase I & II Team;
 RL "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RM Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=2049374; PubMed=11042159;
 RT Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RL "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 RM Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
 RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RL "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer";
 RM Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurohara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohtsuka N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Contains 3 cadherin domains.
 DR EMBL; AK045672; BAC32451.1; -
 DR HSSP; P15116; INCU.
 DR MGD; MGI:2444914; B230220E17R1K.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 3.
 DR PRINTS; PR00205; CADHERIN.

DR SMART; SM00112; CA; 2.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 3.
 KW Calcium; calcium-binding; Hypothetical protein.
 FT NON_TER 337 337
 SQ SEQUENCE 337 AA; 37137 MW; C81B98A3038FA10C CRC64;
 Query Match 90.2%; Score 83; DB 2; Length 337;
 Best Local Similarity 83.3%; Pred. No. 0.00011;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SGSTVTVTLSVDVNDNP 18
 DB 249 SGSTVTVTLSVDVNDNP 266
 RESULT 7
 ID Q6PANA PRELIMINARY; PRT; 508 AA.
 AC Q6PANA;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Adamson R.D., Mulhany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman T.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski J., Skalski D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RL "Generation and initial analysis of more than 15,000 full-length human
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro: IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 4.
 KW Calcium; Calcium-binding.
 SQ SEQUENCE 508 AA; 56368 MW; 9053F774BCF52255 CRC64;
 Query Match 90.2%; Score 83; DB 2; Length 508;
 Best Local Similarity 83.3%; Pred. No. 0.00018;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTVTVTLSVDVNDNP 18

Db 257 SGTTLTTLTVDNDNP 274

RESULT 8
AAH60200 PRELIMINARY; PRT; 508 AA.

ID AAH60200; PRELIMINARY; PRT; 508 AA.
AC 08C375; 01-VAR-2003 (TREMBlrel. 23, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DS Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;

SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanb S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.T., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson W.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravitz M.I., Skalska U., Smalits D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
DR EMBL, BC060200, AAH60200.1, - 9033F774BCF52255 CR664;
SQ SEQUENCE 508 AA; 56388 PM; 9033F774BCF52255 CR664;

Query Match 90.2%; Score 83; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 0.0018;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTYTTLTVDNDNP 18
Db 257 SGTTLTTLTVDNDNP 274

RESULT 9
08C375 PRELIMINARY; PRT; 716 AA.

ID 08C375; 01-VAR-2003 (TREMBlrel. 23, Created)
DT 01-VAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:ID30046N17 product:cadherin 8, full insert
DE sequence.
GN Name=Cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;

SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Head;
MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning";
RT Meth. Enzymol. 303:19-44(1999).
RL Nature 409:685-690(2001).

SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Head;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).

SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Head;
MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Head;
MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaueuchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yonekura Y., Ishikawa T., Ozawa K., Tanaka T., Matsuyama S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichannel sequencer";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasuwa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeya Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Yuramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
(By similarity).
-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC EMBL, AK086711, BAC39724.1, -.

DR HSSP, P15116, INCU.
DR MGD, MGI:107434, Cdh8.
DR GO, GO:0016020, C:membrane, IEA.
DR GO, GO:0005509, F:calcium ion binding, IEA.
DR GO, GO:007156, P:homophilic cell adhesion, IEA.
DR InterPro, IPR002126, Cadherin.
DR InterPro, IPR00233, Cadherin_C_term.
DR Pfam, PF00028, Cadherin_5.
DR Pfam, PF01049, Cadherin_C_1.

DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR DR; PS00268; CADHERIN_2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SO SEQUENCE 716 AA; 79145 MW; 58D598F638624A CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCSTTVTVTLSDVNDNP 18
 ||:||||:||||:||||:
 Db 257 SCSTTVTVTLSDVNDNP 274

RESULT 10
 Q8C449 PRELIMINARY; PRT; 716 AA.
 AC Q8C449;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone: C630002D14 Product: cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RN Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=21085660; PubMed=11217831;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RN Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RT "The FANTOM Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RN Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Kikunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN Integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Fukuda S., Furuno M., Nagata S., Sasaki N., Carninci P.,
 RA Kato H., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bontad M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunatirane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez R., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maier M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.;
 RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL; BC057581; AAH57581.1; -;
 DR EMBL; BC057581; AAH57581.1; -;
 DR HSSP; P15116; INCU.
 DR MGD; MGI:107434; Cdh8.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002326; Cadherin_C-term.
 DR InterPro; IPR002333; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_1; 3.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Transmembrane.
 SO SEQUENCE 716 AA; 79145 MW; 976F5D845F938BD CRC64;

QY 1 SCSTTVTVTLSDVNDNP 18
 ||:||||:||||:||||:
 Query Match 90.2%; Score 83; DB 2; Length 716;
 Best Local Similarity 83.3%; Pred. No. 0.00026;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
DB 257 SGTTLVTTLVDVNDNP 274

RESULT 11
AAH57581 PRELIMINARY; PRT; 716 AA.
ID AAH57581;
AC AAH57581;
DT 02-MAR-2004 (TREMblrel. 27, Created)
DT 02-MAR-2004 (TREMblrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMblrel. 27, Last annotation update)
DE Cdh8 protein.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
OK NCB1_TaxId=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
SQ EMBL: BC057581, AAH57581.1;
SQ SEQUENCE 716 AA; 79145 MW; 976FFSD845F938BD CRC64;

Query Match 90.2%; Score 83; DB 2; Length 716;
Best Local Similarity 83.3%; Pred. No. 0.00026;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTTLVTTLVDVNDNP 18
DB 257 SGTTLVTTLVDVNDNP 274

RESULT 12
Q8BRK4 PRELIMINARY; PRT; 754 AA.
ID Q8BRK4;
AC Q8BRK4;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830035F13 product:cadherin 8, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
OK NCB1_TaxId=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kikunai T., Teshiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishitani T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1157-1171 (2000).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanegaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohata N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira T., Takeeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
DR EMBL: AK044046; BAC11751.1; -.
DR HSSP: P15116; INCU.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR002333; Cadherin_C_term.
DR Pfam: PF00028; Cadherin; 5.
DR PRINTS: PR00205; CADHERIN_C_1.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3
```


DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;

Query Match 90.2%; Score 83; DB 2; Length 754;
 Best Local Similarity 83.3%; Pred. No. 0.00028;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNP 18
 Db 257 SGGTIVTVTLSDVNDNP 274

RESULT 13
 CADI_HUMAN STANDARD; FRT; 790 AA.
 ID CADI_HUMAN
 AC Q13634;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-18 precursor (cadherin-14).
 GN Name=CDH18; Synonyms=CDH14;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184182; PubMed=9030594;
 RA Shibata T., Shimoyama Y., Gotch M., Hirohashi S.;
 RT "Identification of human cadherin-14, a novel neurally specific type,
 RT II cadherin, by protein interaction cloning.";
 RL J. Biol. Chem. 272:5236-5240(1997).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U59325; AAB02933.1; -
 DR PIR; G02678; G02678.
 DR HSSP; P09803; 117X.
 DR GeneW; HGNC:1757; CDH18.
 DR MIM; 603019; -
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000333; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 790 Cadherin-18.
 FT DOMAIN 54 608 Extracellular (Potential).
 FT TRANSMEM 609 636 Potential.
 FT DOMAIN 637 790 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.

FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 790 AA; 88072 MW; 5C7BDEB229B6EDCA CRC64;

Query Match 90.2%; Score 83; DB 1; Length 790;
 Best Local Similarity 83.3%; Pred. No. 0.0003;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNP 18
 Db 249 SGGTIVTVTLSDVNDNP 266

RESULT 14
 CADH_HUMAN STANDARD; FRT; 799 AA.
 ID CADH_HUMAN
 AC P5286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=CDH8
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=10861224;
 RX Shimoyama Y., Tsujimoto G., Kitaajima M., Natori M.;
 RA "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins.";
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin.";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue.";
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC


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DR EMBL: AB035305; BAB7419.1; -.
DR EMBL: U34060; AAA35628.1; ALT_INIT.
DR HSSP: P09803; 117W.
DR Genew: HGNC:1767; CDH8.
DR MIM: 603008; -.
DR GO: GO:0007155; P:cell adhesion; TAS.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 61 Potential.
FT CHAIN 62 799 Cadherin-8.
FT DOMAIN 62 621 Extracellular (Potential).
FT TRANSMEM 622 642 Potential.
FT DOMAIN 643 799 Cytoplasmic (Potential).
FT DOMAIN 643 799 Cadherin 1.
FT DOMAIN 168 276 Cadherin 2.
FT DOMAIN 277 391 Cadherin 3.
FT DOMAIN 392 494 Cadherin 4.
FT DOMAIN 495 616 Cadherin 5.
FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
SQ SEQUENCE 799 AA; 88253 MW; 9B1198B6039C6A0A CRC64;

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.0003;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTTVTLSPVNDNP 18
DB 257 SGTTLTLTLVDVNDNP 274

RESULT 15
CAD8 MOUSE STANDARD; PRT; 799 AA.
AC 297251;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-8 precursor.
GN Name=Cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Swiss Webster / NIH;
RX MEDLINE=97174321; Pubmed=9022055;
RA Korematsu K., Redies C.;
RT "Restricted expression of cadherin-8 in segmental and functional
subdivisions of the embryonic mouse brain.";
RL Dev. Dyn. 208:178-189(1997).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 5 cadherin domains.

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CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL: X95600; CAA64857.1; -.
DR HSSP: P09803; 117W.
DR MGD: MG1:107434; Cdh8.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SMO0112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 61 Potential.
FT CHAIN 62 799 Cadherin-8.
FT DOMAIN 62 621 Extracellular (Potential).
FT TRANSMEM 622 642 Potential.
FT DOMAIN 643 799 Cytoplasmic (Potential).
FT DOMAIN 643 799 Cadherin 1.
FT DOMAIN 168 276 Cadherin 2.
FT DOMAIN 277 391 Cadherin 3.
FT DOMAIN 392 494 Cadherin 4.
FT DOMAIN 495 616 Cadherin 5.
FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.0003;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTTVTLSPVNDNP 18
DB 257 SGTTLTLTLVDVNDNP 274

Search completed: December 8, 2004, 10:24:39
Job time : 8.21488 secs

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transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancer, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA:

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 1 SGGTIVTVTLSDVNDNPP 18

RESULT 2

ADD29452
ID ADD29452 standard; peptide; 18 AA.

AC ADD29452;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein peptide fragment Seq ID11.

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.

OS Homo sapiens.

PN US2003144491-A1.

PD 31-JUL-2003.

PF 16-FEB-2001; 2001US-00786051.

PR 03-FEB-2000; 2000US-00486914.
PR 27-APR-2000; 2000US-00560875.

PA (GDB/) GDBOLE S D.

PA (KDOC/) KIO C.

PA (ARTE/) ARTERBURN M C.

PA (YERN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LUC/) LIU C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancer, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX Claim 11; SEQ ID NO 11; 63pp; English.
CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-

cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancer, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA:

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 1 SGGTIVTVTLSDVNDNPP 18

RESULT 3

AD116946
ID AD116946 standard; protein; 493 AA.

AC AD116946;

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue SegID 482.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

XX inflammation; autoimmune disorder; allergy; blood disorder;

XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;

XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;

XX Alzheimer's disease; infection; str.

OS Homo sapiens.

PN WO200268649-A2.

PD 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 31-JAN-2001; 2001US-0265517P.

PR 02-FEB-2001; 2001US-0266406P.

PR 05-FEB-2001; 2001US-0266767P.

PR 07-FEB-2001; 2001US-0266975P.

PR 07-FEB-2001; 2001US-0267057P.

PR 08-FEB-2001; 2001US-0267459P.

PR 09-FEB-2001; 2001US-0267823P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 27-FEB-2001; 2001US-0271855P.

PR 02-MAR-2001; 2001US-0272788P.

PR 02-MAR-2001; 2001US-0273046P.

PR 14-MAR-2001; 2001US-0275925P.

PR 14-MAR-2001; 2001US-0275947P.

PR 14-MAR-2001; 2001US-0275950P.

PR 14-MAR-2001; 2001US-0275989P.

PR 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.

PR 16-MAR-2001; 2001US-0276397P.

PR 16-MAR-2001; 2001US-0276768P.

PR 20-MAR-2001; 2001US-0278652P.

PR 26-MAR-2001; 2001US-0278775P.

PR 26-MAR-2001; 2001US-0278778P.

PR 29-MAR-2001; 2001US-0279882P.

PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282929P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 20-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0315447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 12-SEP-2001; 2001US-0318140P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

PI Therney VT, Spylex KA, Zernhusen BD, Paturaajan M, Shinkets RA;
 PI Li L, Gargolli BA, Padigar M, Anderson DM, Rastelli L, Miller CE;
 PI Getlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CEA;
 PI Furrak K, Grosse WM, Alsdbrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX WPI; 2002-706998/76.

PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

PS Disclosure; SEQ ID NO 482; 1498bp; English.

CC This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytostatic, cardiant, antiinflammatory, immunosuppressive, anti-allergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antisthmatic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.

XX Sequence 493 AA;

Query Match

100.0%; Score 92; DB 5; Length 493;

Best Local Similarity 100.0%; Pred. NO. 5.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTVTVTLSPDNDNP 18
 Db 240 SGGSTVTVTLSPDNDNP 257

RESULT 4
 ABB53295
 ID ABB53295 standard; protein; 607 AA.
 XX ABB53295;
 AC ABB53295;
 DT 12-FEB-2002 (first entry)
 XX
 DE Human polypeptide #35.

XX Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquilizer; antiarrhythmic; cardiant; antisthmatic;
 KW antiinflammatory; antidiabetic; hepatotropic; virucide; antidiabetic;
 KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199633P.

XX 11-MAY-2000; 2000US-020336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kohnick KS;
 PI Lal Y, Xie Q;
 XX WPI; 2002-041392/05.
 DR N-PSDB; ABA90360.

PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PS Claim 1; Page 106-108; 116bp; English.

CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases

CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility, and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention
 XX
 SQ Sequence 607 AA;

Query Match 100.0%; Score 92; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 7e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSDVNDNP 18
 |||||
 DB 240 SGGSTVTVTLSDVNDNP 257

RESULT 5

ADD29448
 ID ADD29448 standard; protein; 620 AA.

AC ADD29448;
 XX

DT 15-JAN-2004 (first entry)
 XX

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;
 XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
 XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 XX metastatic tumour; human.

OS Homo sapiens.

PN US200314491-A1.

PD 31-JUL-2003.

PE 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LITC/) LIT C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

PT Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

PS Claim 11; SEQ ID NO 7; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may
 CC allow development of therapeutic useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the mature human secreted

CC cadherin-like protein which was used during the exemplification of the
 CC invention.
 CC
 SQ Sequence 620 AA;

Query Match 100.0%; Score 92; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 7.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTVTVTLSDVNDNP 18
 |||||
 DB 224 SGGSTVTVTLSDVNDNP 241

RESULT 6

ADD29445
 ID ADD29445 standard; protein; 636 AA.

AC ADD29445;
 XX

DT 15-JAN-2004 (first entry)
 XX

DE Human cadherin-like protein amino acid sequence.

XX cadherin-like protein; transmembrane protein; cadherin domain;

XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;

XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 XX metastatic tumour; human.

OS Homo sapiens.

PN US200314491-A1.

PD 31-JUL-2003.

PE 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LITC/) LIT C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

PT Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

PS Claim 11; SEQ ID NO 4; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
 CC protein and the DNA sequence which encodes it. Cadherins are a family of
 CC transmembrane proteins which share a common cadherin domain in their
 CC extracellular region. The extracellular portion mediates homotypic cell-
 CC cell adhesion that is calcium dependent. Modulators of the protein of the
 CC invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

CC Sequence 636 AA;

Query Match 100.0%; Score 92; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTYVTLSDVNDNPP 18
DB 240 SGGTTVTYVTLSDVNDNPP 257

RESULT 7
ABBS3296
ID ABB53296 standard; protein; 781 AA.

AC ABB53296;
XX
DT 12-FEB-2002 (first entry)

XX Human polypeptide #36.

XX Human; nociceptive; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; anticholinergic; cardiac; antidiabetic;
XX antiinflammatory; antihypertensive; hepatotropic; vincicide; antidiabetic;
XX nephrotropic; anorectic; cytosstatic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

XX 11-MAY-2000; 2000US-0203336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Aggarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnick KS;

XX Lai Y, Xie Q;

XX WPI; 2002-041392/05.

XX N-PSDB; ABA90361.

XX Claim 1; Page 108-109; 116pp; English.

CC The invention relates to an isolated polypeptide comprising a 277, 480,
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
CC 844, 782, 262, 394, 471, 485, 286, 513, 495, 350, 619, 490, 462, 285,
CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
CC given in the specification. The polypeptides, modulators of the
CC polypeptides and antibodies against the polypeptides are useful for
CC treating diseases such as neurological and psychiatric diseases including
CC Alzheimer's, paraspinal nerve palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including

CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Ehlerburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including
CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention

CC Sequence 781 AA;

Query Match 100.0%; Score 92; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTYVTLSDVNDNPP 18
DB 240 SGGTTVTYVTLSDVNDNPP 257

RESULT 8
AAM48736
ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

XX 28-MAR-2002 (first entry)

XX Human cadherin family member 57805, protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
XX antidiabetic; neuroprotective; antiarthritic; antineuritic;
XX dermatological; immunosuppressive; antiinflammatory; antipsoriatic;
XX antiaesthetic; antiallergic; antileptotic; haemostatic; antipruritic;
XX antihypertensive; antihypertensive; cardiac; anticholinergic;
XX anorectic; immunomodulatory; vasotropic; vincicide; cytosstatic; liver;
XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
XX gene therapy.

XX Homo sapiens.

XX WO200190145-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016013.

XX 19-MAY-2000; 2000US-0205674P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtiss RAJ;

XX WPI; 2002-083082/11.

XX N-PSDB; ABA96406, ABA96407.

CC New human cadherin family protein and polynucleotides, useful for
CC diagnosing and treating disorders e.g. obstructive jaundice, multiple
CC sclerosis, encephalomyelitis and atherosclerosis and to identify
CC modulators of therapeutic use.
CC Claim 9; Page 105; 119pp; English.
CC The invention relates to human cadherin family polypeptide designated

01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Pilvaroff E, Goddard A, Grimaldi JC,
PI Gunney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX
DR WP1: 2002-362426/39.
DR N-PDSB; ABK70009.
XX
FT New PRO polypeptides and polynucleotides encoding the polypeptides,
FT useful in gene therapy, chromosome identification, tissue typing, or for
FT genetic analysis of individuals with genetic disorders.
PS
PS Claim 11, Fig 98; 218pp; English.

This invention relates to the cDNA and protein sequences of novel secreted and transmembrane polypeptides PRO polypeptides. The invention also comprises a method for producing the proteins of the invention by recombinant means and antibodies specific for the protein of the invention. The antibody may be used for detecting the PRO proteins of the invention and may be used to modify their activity. Polynucleotides may be used as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, to construct hybridisation probes for mapping the gene which encodes that PRO and for genetic analysis of individuals with genetic disorders, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knock-out animals which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in cancerous tumors and for screening for differentially expressed genes using microarray technology. The present sequence represents a human PRO protein of the invention

Sequence 781 AA;

Query Match 100.0%; Score 92; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 9,5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTTVTLSDVNDNP 18
DB 240 SGSTTVTLSDVNDNP 257
|||||
|||

RESULT 10
AD116604
ID AD116604 standard; protein: 781 AA.
XX
AC AD116604;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein to treat human pathological conditions SeqID140.

KM human; NOVA; cardiomyopathy; atherosclerosis; cancer; diabetes;
KM inflammation; autoimmune disorder; allergy; blood disorder;
KM acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KM immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KM Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KM cytostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
KM haemostatic; anti-HIV; antidiabetic; antileukosclerotic; anorectic;
KM antilastmatic; nephrotropic; antiarrhythmic; hepatotropic;
KM neuroprotective; nootropic; antibacterial; virocidic; antiparasitic;
KM relevant; anticoinvulsant; neurogenesis; wound healing; angiogenesis;
KM chromosome mapping; tissue typing; pharmacogenomic; SNP;
KM single nucleotide polymorphism.

XX Homo sapiens.
XX WO200268649-A2.
XX 06-SEP-2002.
XX 31-JAN-2002; 2002WO-US002795.
XX 31-JAN-2001; 2001US-0265399P.
XX 31-JAN-2001; 2001US-0265419P.
XX 31-JAN-2001; 2001US-0265519P.
XX 31-JAN-2001; 2001US-0265519P.
XX 02-FEB-2001; 2001US-0266406P.
XX 05-FEB-2001; 2001US-0266767P.
XX 07-FEB-2001; 2001US-0266975P.
XX 07-FEB-2001; 2001US-0267057P.
XX 08-FEB-2001; 2001US-0267459P.
XX 09-FEB-2001; 2001US-0267823P.
XX 15-FEB-2001; 2001US-0268974P.
XX 26-FEB-2001; 2001US-0271664P.
XX 27-FEB-2001; 2001US-0271839P.
XX 02-MAR-2001; 2001US-0272788P.
XX 02-MAR-2001; 2001US-0273046P.
XX 14-MAR-2001; 2001US-0275925P.
XX 14-MAR-2001; 2001US-0275947P.
XX 14-MAR-2001; 2001US-0275950P.
XX 14-MAR-2001; 2001US-0275959P.
XX 15-MAR-2001; 2001US-0276448P.
XX 15-MAR-2001; 2001US-0276450P.
XX 16-MAR-2001; 2001US-0276397P.
XX 20-MAR-2001; 2001US-0276529P.
XX 26-MAR-2001; 2001US-0276775P.
XX 26-MAR-2001; 2001US-0276788P.
XX 29-MAR-2001; 2001US-0279882P.
XX 29-MAR-2001; 2001US-0279884P.
XX 30-MAR-2001; 2001US-0280147P.
XX 11-APR-2001; 2001US-0282992P.
XX 11-APR-2001; 2001US-0283083P.
XX 20-APR-2001; 2001US-0285133P.
XX 23-APR-2001; 2001US-0285749P.
XX 03-MAY-2001; 2001US-0286327P.
XX 03-MAY-2001; 2001US-0286504P.
XX 29-MAY-2001; 2001US-0294047P.
XX 30-MAY-2001; 2001US-0294473P.
XX 08-JUN-2001; 2001US-0296964P.
XX 18-JUN-2001; 2001US-0298959P.
XX 19-JUN-2001; 2001US-0299324P.
XX 13-AUG-2001; 2001US-0312020P.
XX 16-AUG-2001; 2001US-0312889P.
XX 16-AUG-2001; 2001US-0312898P.
XX 21-AUG-2001; 2001US-0313390P.
XX 28-AUG-2001; 2001US-0315470P.
XX 31-AUG-2001; 2001US-0316447P.
XX 07-SEP-2001; 2001US-0318115P.
XX 07-SEP-2001; 2001US-0318118P.
XX 12-SEP-2001; 2001US-0318740P.
XX 19-SEP-2001; 2001US-0323797P.
XX 18-OCT-2001; 2001US-0330245P.
XX 18-OCT-2001; 2001US-0330308P.
XX 14-NOV-2001; 2001US-0332701P.
XX (CURA-) CURAGEN CORP.
XX Therneve VT, Spytek KA, Ze-husen BD, Patturajan M, Shinkels RA,
XX Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE,
XX Gerlach VL, Taupier RJ, Gueev VY, Colman SD, Wolenc AR, Pena CE,
XX Futrak K, Grose WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE,
XX WPI; 2002-706998/76.
XX N DCS 1016603

XX New NOVX polypeptides and nucleic acids, useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, cardiovascularity,
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX Claim 1; SEQ ID NO 140; 1498bp; English.
XX
XX This invention relates to a novel nucleic acid, and encoded polypeptides
XX thereof, which have properties related to the stimulation of biochemical
XX or physiological responses in a cell, tissue, organ or organism.
XX Specifically, it refers to the use of biologically active fragments for
XX diagnostic and prognostic assays and furthermore in the treatment of
XX diverse pathological conditions. The present invention describes novel
XX human and murine NOVX proteins, as well as methods to modulate their
XX expression using antisense oligos, ribozymes and peptide nucleic acids.
XX The NOVX polypeptides, polynucleotides and antibodies are useful in
XX treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
XX atherosclerosis, cancer and diabetes. Furthermore, they may be used in
XX treating or preventing diseases such as inflammation, autoimmune
XX disorders, allergies, blood disorders, acquired immunodeficiency syndrome
XX (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
XX arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
XX and epilepsy. Accordingly, these molecules have many activities including
XX cytoskeletal, cardiant, antiinflammatory, immunosuppressive, antiallergic,
XX haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
XX antisthmatic, nephrotropic, antiarthritic, hepatotropic,
XX neuroprotective, nootropic, antibacterial, virotoxic, antiparasitic,
XX relaxant and anticoagulant. In addition, they are useful in screening
XX assays to identify small molecules that modulate or inhibit, for example,
XX neurogenesis, wound healing and angiogenesis. The nucleic acids are also
XX used as in chromosome mapping, tissue typing, preventive medicine and
XX pharmacogenomics. This polypeptide is a human NOVX protein of the
XX invention.
XX
XX Sequence 781 AA:
XX
XX Query Match 100.0%; Score 92; DB 5; Length 781;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-06;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGGTTVTVLSDVNDNP 18
XX DB 240 SGGTTVTVLSDVNDNP 257
XX
XX RESULT 11
XX AD116606
XX ID AD116606 standard; protein; 781 AA.
XX
XX AC AD116606;
XX
XX DT 15-APR-2004 (first entry)
XX
XX DE Human NOVX protein to treat human pathological conditions SeqID142.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;
XX immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cycostatic; cardiant; antiinflammatory; immunosuppressive; anorectic;
XX haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
XX antiasthmatic; nephrotropic; antiarthritic; hepatotropic;
XX neuroprotective; nootropic; antibacterial; virotoxic; antiparasitic;
XX relaxant; anticoagulant; neurogenesis; wound healing; angiogenesis;
XX chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
XX WO200268649-A2.
XX 06-SEP-2002.

PR 21-SEP-2001; 2001US-0324781P.
PR 05-OCT-2001; 2001US-0327606P.
PR 12-OCT-2001; 2001US-0328960P.
PR 09-NOV-2001; 2001US-0344471P.
PR 17-MAY-2002; 2002US-0381291P.
XX
XX
XX (INCYTE GENOMICS INC.)
XX Burford N, Warren BA, Duggan BM, Mason EM, Richardson TM, Yue H;
XX Forsythe JD, Elliott VS, Griffith JA, Gorvad AE, Azimzai Y;
XX Kallik DA, Xu Y, Honchell CD, Baughn MR, Glezen KJ, Lee S;
XX Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
XX WPI: 2003-354645/33.
XX N-PSDB: ACC0402.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
XX useful for diagnosing, treating or preventing disorders associated with
XX aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
XX or stroke.
XX
XX Claim 1; Page 192-194; 234pp; English.
XX
XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACCC0392-ACCC0413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
XX syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
XX lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
XX proliferative disorders (e.g. cancer or atherosclerosis)
XX
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTTVTLSDVNDNPP 18
DB 240 SGGSTTVTLSDVNDNPP 257
RESULT 13
ADA01366
ID ADA01366 standard; protein; 781 AA.
XX
XX ADA01366;
XX
XX 06-NOV-2003 (first entry)
XX
XX Human PRO polypeptide #49.
DE
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteoporosis; antirheumatic; antiarthritic.
XX
XX Homo sapiens.
XX
XX US2003068779-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX

XX (SETH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX
XX WPI: 2003-625484/59.
XX N-PSDB: ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for inducing endothelial cell
XX tube formation and for treating sports-related joint problems, articular
XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
XX represents a human PRO polypeptide of the invention.
XX
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTTVTLSDVNDNPP 18
DB 240 SGGSTTVTLSDVNDNPP 257
RESULT 14
ADA43795
ID ADA43795 standard; protein; 781 AA.
XX
XX ADA43795;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human secreted/transmembrane polypeptide PRO34009.
DE
XX
XX Human; PRO; secreted protein; transmembrane protein;
XX microvascular endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
XX
XX US2003064474-A1.
XX
XX 03-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245859.
XX

XX 29-JUL-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GENTH) GENENTECH INC.
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI; 2003-605867/57.
 DR N-PDB; ADA43562.
 XX
 PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 11; Fig 98; 308pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO1207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 92; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTTVTVLSDVNDNP 18
 Db 240 SGGTTVTVLSDVNDNP 257
 RESULT 15
 ADA43563
 ID ADA43563 standard; protein; 781 AA.
 XX
 AC ADA43563;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX

KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 FN US2003073196-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 18-SEP-2002; 2002US-00246210.
 XX
 XX 04-APR-2001; 2001US-0282199.
 PR 29-AUG-2001; 2001MO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX WPI; 2003-743814/70.
 DR N-PDB; ADA43562.
 XX
 PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
 PT PRO21383 useful for stimulating the proliferation or differentiation of
 PT chondrocyte cells and detecting the presence of a tumor in a mammal.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
 CC PRO10275, PRO1207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.
 XX
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 92; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTTVTVLSDVNDNP 18

Wed Dec 8 11:46:20 2004

us-09-788-051-11.rag

Page 11

Db 240 SGSTVTVTLSDVNDNDPP 257

Search completed: December 8, 2004, 10:13:06
Job time : 8.44864 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 : Search time 18.3932 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-11
Perfect score: 92
Sequence: 1 SGSTVTVTLSVDVNDNP 18

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	18	10	US-09-788-051-11
2	92	100.0	18	10	US-09-788-051-12
3	92	100.0	493	15	US-10-072-012-482
4	92	100.0	607	15	US-10-258-851-74
5	92	100.0	620	10	US-09-788-051-7
6	92	100.0	636	10	US-09-788-051-4
7	92	100.0	781	9	US-09-860-868-2
8	92	100.0	781	14	US-10-245-752-98
9	92	100.0	781	14	US-10-245-859-98
10	92	100.0	781	14	US-10-245-103-98
11	92	100.0	781	14	US-10-245-107-98
12	92	100.0	781	14	US-10-245-143-98
13	92	100.0	781	14	US-10-245-771-98

14	92	100.0	781	14	US-10-245-851-98	Sequence 98, Appl
15	92	100.0	781	14	US-10-245-883-98	Sequence 98, Appl
16	92	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
17	92	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
18	92	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
19	92	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
20	92	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
21	92	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
22	92	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
23	92	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
24	92	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
25	92	100.0	781	14	US-10-239-196-98	Sequence 98, Appl
26	92	100.0	781	14	US-10-243-024-98	Sequence 98, Appl
27	92	100.0	781	14	US-10-243-409-98	Sequence 98, Appl
28	92	100.0	781	14	US-10-245-621-98	Sequence 98, Appl
29	92	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
30	92	100.0	781	14	US-10-245-033-98	Sequence 98, Appl
31	92	100.0	781	14	US-10-243-095-98	Sequence 98, Appl
32	92	100.0	781	14	US-10-245-185-98	Sequence 98, Appl
33	92	100.0	781	14	US-10-245-427-98	Sequence 98, Appl
34	92	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
35	92	100.0	781	14	US-10-245-770-98	Sequence 98, Appl
36	92	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
37	92	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
38	92	100.0	781	14	US-10-243-320-98	Sequence 98, Appl
39	92	100.0	781	14	US-10-162-435-13	Sequence 13, Appl
40	92	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
41	92	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
42	92	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
43	92	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
44	92	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
45	92	100.0	781	14	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-11
Sequence 11, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenhua
APPLICANT: Dimarac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-11

Query Match 100.0%; Score 92; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SGSTVTVTLSVDVNDNP 18

Db 1 SGSTTVTVTLSDVNDNP 18

RESULT 2

US-09-788-051-12
Sequence 12, Application US/09788051
Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chia-Yun
APPLICANT: Artebarrin, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: HVS-39
CURRENT APPLICATION NUMBER: US/09/788, 051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-12

Query Match

Best Local Similarity 100.0%; Score 92; DB 10; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTTVTVTLSDVNDNP 18

Db 1 SGSTTVTVTLSDVNDNP 18

RESULT 3

US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar
APPLICANT: Seytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkels, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grose, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012

Db 1 SGSTTVTVTLSDVNDNP 18

RESULT 4

US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Kahnick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50025
CURRENT APPLICATION NUMBER: US/10/258, 951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 240 SGSTTVTVTLSDVNDNP 257

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 240 SGGTTVTTLSDVNDNP 257

RESULT 5
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimane, Radjo T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 92; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 224 SGGTTVTTLSDVNDNP 241

RESULT 6
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimane, Radjo T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HVS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0

; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

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Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 240 SGGTTVTTLSDVNDNP 257

RESULT 7
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-860-868-2

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Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNP 18
DB 240 SGGTTVTTLSDVNDNP 257

RESULT 8
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Den
; APPLICANT: Rivaroli, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24

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/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: prt
/ ORGANISM: Homo Sapien
US-10-245-752-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGGTGTGTTGSDVNDNPP 18
Db      240  GGGTGTGTTGSDVNDNPP 257

RESULT 9
US-10-245-859-98
/ Sequence 98, Application US/10245859
/ Publication No. US20030064474A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245, 859
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: prt
/ ORGANISM: Homo Sapien
US-10-245-859-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGGTGTGTTGSDVNDNPP 18
Db      240  GGGTGTGTTGSDVNDNPP 257

RESULT 10
US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication No. US20030068778A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C112
/ CURRENT APPLICATION NUMBER: US/10/245, 103
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: prt
/ ORGANISM: Homo Sapien
US-10-245-103-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGGTGTGTTGSDVNDNPP 18
Db      240  GGGTGTGTTGSDVNDNPP 257
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Db 240 SGGTTVTVTLSDVNDNP 257

RESULT 11

US-10-245-107-98

Sequence 98, Application US/10245107
Publication No. US2003006879A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watambe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C71
CURRENT APPLICATION NUMBER: US/10/245,107
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-107-98

US-10-245-107-98

Query Match 100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNP 18

Db 240 SGGTTVTVTLSDVNDNP 257

RESULT 12

US-10-245-143-98

Sequence 98, Application US/10245143
Publication No. US20030068780A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watambe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C90
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 98
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNP 18

Db 240 SGGTTVTVTLSDVNDNP 257

RESULT 13

US-10-245-771-98

Sequence 98, Application US/10245771
Publication No. US20030068781A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watambe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C98
CURRENT APPLICATION NUMBER: US/10/245,771
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTWTYTLSPVDNDNP 18
Db 240 SGGTWTYTLSPVDNDNP 257

RESULT 14
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC93
; CURRENT APPLICATION NUMBER: US/10/245, 851
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTWTYTLSPVDNDNP 18
Db 240 SGGTWTYTLSPVDNDNP 257

RESULT 15
US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC70
; CURRENT APPLICATION NUMBER: US/10/245, 883
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Wed Dec 8 11:46:20 2004

us-09-788-051-11.rapb

Page 7

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|||
Db 240 SGTITVTVTLSDVNDNPP 257
|||

Search completed: December 8, 2004, 11:34:29
Job time : 18.3932 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 2.1464 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-11

Perfect score: 92

Sequence: 1 SGSTVTVTLSDVNDNPP 18

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Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/BACKFILES.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	90.2	109	3	US-09-187-859-17
2	83	90.2	109	4	US-09-839-542B-17
3	83	90.2	109	4	US-09-535-852-17
4	83	90.2	532	1	US-08-188-228-44
5	83	90.2	532	1	US-08-332-638-44
6	83	90.2	793	1	US-08-188-228-54
7	83	90.2	793	1	US-08-332-643-48
8	83	90.2	793	1	US-08-332-638-54
9	83	90.2	799	1	US-08-188-228-42
10	83	90.2	799	1	US-08-332-638-42
11	82	89.1	109	4	US-09-187-859-11
12	82	89.1	109	4	US-09-839-542B-11
13	82	89.1	109	4	US-09-535-852-11
14	80	87.0	109	3	US-09-187-859-23
15	80	87.0	109	4	US-09-187-859-23
16	80	87.0	109	4	US-09-839-542B-8
17	80	87.0	109	4	US-09-839-542B-23
18	80	87.0	109	4	US-09-535-852-8
19	80	87.0	109	4	US-09-535-852-23
20	80	87.0	653	1	US-08-188-228-46
21	80	87.0	653	1	US-08-332-638-46
22	79	85.9	109	3	US-09-187-859-5
23	79	85.9	109	3	US-09-839-542B-5
24	79	85.9	109	4	US-09-535-852-5
25	79	85.9	635	2	US-08-738-349-12
26	79	85.9	635	2	US-08-738-349-6
27	79	85.9	693	4	US-09-919-497-55

28	79	85.9	796	1	US-08-188-228-58	Sequence 58, Appl
29	79	85.9	796	1	US-08-332-643-52	Sequence 52, Appl
30	79	85.9	796	1	US-08-332-638-58	Sequence 58, Appl
31	79	85.9	796	2	US-08-738-349-2	Sequence 2, Appl
32	79	85.9	796	2	US-08-738-349-4	Sequence 4, Appl
33	79	85.9	796	4	US-09-654-328-2	Sequence 15, Appl
34	71	77.2	109	3	US-09-187-859-15	Sequence 15, Appl
35	71	77.2	109	4	US-09-839-542B-15	Sequence 15, Appl
36	71	77.2	109	4	US-09-535-852-15	Sequence 15, Appl
37	71	77.2	794	1	US-08-188-228-60	Sequence 60, Appl
38	71	77.2	794	1	US-08-332-643-54	Sequence 54, Appl
39	71	77.2	794	1	US-08-332-638-60	Sequence 60, Appl
40	62	67.4	148	1	US-07-998-003A-36	Sequence 36, Appl
41	62	67.4	148	1	US-08-453-274B-36	Sequence 36, Appl
42	62	67.4	148	1	US-08-453-695A-36	Sequence 36, Appl
43	62	67.4	148	1	US-08-268-161A-36	Sequence 36, Appl
44	62	67.4	148	2	US-08-453-702A-36	Sequence 36, Appl
45	62	67.4	148	3	US-09-099-639-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-187-859-17
Sequence 17, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-17

Query Match 90.2%; Score 83; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

QY 1 SGSTVTVTLSDVNDNPP 18
DB 90 SGSTVTVTLSDVNDNPP 107

RESULT 2
US-09-839-542B-17
Sequence 17, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-839-542B-17

Query Match 90.2%; Score 83; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDNDNP 18
|||||:|||||
Db 90 SGGTWTVTLSVDNDNP 107

RESULT 3
US-09-535-852-17
; Sequence 17, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.4076
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-852-17

Query Match 90.2%; Score 83; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDNDNP 18
|||||:|||||
Db 90 SGGTWTVTLSVDNDNP 107

RESULT 4
US-08-188-228-44
; Sequence 44, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-44

Query Match 90.2%; Score 83; DB 1; Length 532;
Best Local Similarity 83.3%; Pred. No. 6.7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDNDNP 18
|||||:|||||
Db 257 SGGTWTVTLSVDNDNP 274

RESULT 5
US-08-332-638-44
; Sequence 44, Application US/08332638
; Patent No. 5646250
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-44

Query Match 90.2%; Score 83; DB 1; Length 532;
Best Local Similarity 83.3%; Pred. No. 6.7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDNDNP 18

Db 257 SGTTLVTLTDVNDNP 274

RESULT 6

US-08-188-228-54
Sequence 54, Application US/08188228

Patent No. 569725

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,228

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/049,460

FILING DATE: 19 APR 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 569725and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-188-228-54

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTTLVTLTDVNDNP 18
Db 250 SGTTLVTLTDVNDNP 267

RESULT 7

US-08-332-643-48
Sequence 48, Application US/08332643

Patent No. 563634

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 564625and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-643-48

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTTLVTLTDVNDNP 18
Db 250 SGTTLVTLTDVNDNP 267

RESULT 8

US-08-332-638-54
Sequence 54, Application US/08332638

Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 564625and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-643-48

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/872,643

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5639634and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ. ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-643-48

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDVNDNP 18
Db 250 SGTTLVTTLTDVNDNP 267

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19-APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDVNDNP 18
Db 257 SGTTLVTTLTDVNDNP 274

RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTWTVTLSVDVNDNP 18
Db 257 SGTTLVTTLTDVNDNP 274

RESULT 11
US-09-187-859-11
Sequence 11, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-187-859-11

Query Match 89.1%; Score 82; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
DB 90 SGTISVTITLDVNDNPP 107

RESULT 12

US-09-839-542B-11
Sequence 11, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-839-542B-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
DB 90 SGTISVTITLDVNDNPP 107

RESULT 13

US-09-535-852-11
Sequence 11, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-535-852-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18

DB 90 SGTISVTITLDVNDNPP 107

RESULT 14
US-09-187-859-8
Sequence 8, Application US/09187859A
Patent No. 6358920

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 109
TYPE: PRT

ORGANISM: Homo sapiens
US-09-187-859-8

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
DB 90 SGTIVNITITLDVNDNPP 107

RESULT 15

US-09-187-859-23
Sequence 23, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 109
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-187-859-23

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
DB 90 SGTIVTITVITLDVNDNPP 107

Search completed: December 8, 2004, 10:01:13
Job time : 2.1464 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.45573 Seconds
(without alignments)

1189.717 Million cell updates/sec

Title: US-09-788-051-12

Perfect score: 92

Sequence: 1 SGGTIVTILSDVNDNPP 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	90.2	790	2	G02678
2	83	90.2	793	2	D38992
3	82	89.1	785	2	I50180
4	81	88.0	790	2	I51638
5	80	87.0	789	2	I52701
6	80	87.0	790	2	I50178
7	80	87.0	790	2	I37016
8	79	85.9	796	2	A38992
9	79	85.9	796	2	I48277
10	79	85.9	796	2	I49556
11	79	85.9	796	2	A53584
12	71	77.2	794	2	I59372
13	67	72.8	2809	2	T30213
14	65	70.7	4351	2	T00252
15	62	67.4	784	1	IUHUC5
16	62	67.4	877	1	IUHUCN
17	62	67.4	906	1	IUHUCN
18	62	67.4	906	1	IUHUCN
19	62	67.4	912	1	IUHUCN
20	61	66.3	913	1	IUHUCN
21	61	66.3	913	1	IUHUCN
22	61	66.3	913	1	IUHUCN
23	58	63.0	2610	2	T20968
24	57	62.0	4307	2	T20721
25	57	62.0	773	2	B38992
26	57	62.0	770	2	B48910
27	57	62.0	840	2	I37281
28	57	62.0	894	2	I37282
29	57	62.0	905	1	IUHUC1

30	57	62.0	906	1	IUHUC2	N-cadherin 2 precu
31	57	62.0	1715	2	TJ0128	Bombay mori recept
32	57	62.0	3097	2	T00021	DN-cadherin - fru
33	57	62.0	3147	1	IUHUCN	cadherin-related t
34	56	60.9	373	2	I34563	hypothetical prote
35	56	60.9	882	1	IUHUC5	cadherin 1 precurs
36	56	60.9	1069	2	T00043	BH-protocadherin-a
37	56	60.9	1072	2	T00041	BH-protocadherin p
38	56	60.9	1200	2	T00042	T-cadherin precurs
39	55	59.8	712	1	IUHUCN	T-cadherin 2 - chi
40	55	59.8	717	2	I51206	desmocollin - boyl
41	55	59.8	886	2	I45858	seven-pass transme
42	55	59.8	3034	2	I14119	desmocollin, type
43	54	58.7	826	2	B55363	desmocollin, type
44	54	58.7	896	2	A55363	cadherin 4 precurs
45	54	58.7	916	2	C38992	

ALIGNMENTS

RESULT 1
G02678
cadherin-14 - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C/Accession: G02678
R/Shibata, T.; Shimoyama, Y.; Gotoh, N.; Hirohashi, S.
Submitted to the EMBL Data Library, May 1996
A/Reference number: H01584
A/Accession: G02678
A/Molecule type: mRNA
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Residues: 1-790 <SHI>
A/Cross-references: UNIPROT:Q13614; EMBL:U59325; NID:g1389652; PDB:AA02933.1; PDB:g13
C/Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTILSDVNDNPP 18
DB 249 SGGTIVTILSDVNDNPP 266

RESULT 2
D38992
cadherin 8 - human
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C/Accession: D38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MIMD:91283540; PMID:2059658
A/Accession: D38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-793 <SUZ>
A/Cross-references: GB:I34060; NID:g506411; PID:AAA5628.1; PID:g506412
A/Genes: GDB:CDH8
C/Cross-references: GDB:5822911
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 90.2%; Score 83; DB 2; Length 793;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTTVTTLTSDVNDNPP 18
||:||||:|||||
Db 250 SGTTLTTLTLDVNDNPP 267

RESULT 3

150180
C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: 150180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec
A/Reference number: 150178; PMID:95309115; PMID:7540531
A/Accession: 150180
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-785 <NA>
A/Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 89.1%; Score 82; DB 2; Length 785;
Best Local Similarity 83.3%; Pred. No. 7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTTVTTLTSDVNDNPP 18
||:||||:|||||
Db 243 SGTTLTTLTLDVNDNPP 260

RESULT 4

151638
F:cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: 151638; S55381
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A>Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A/Reference number: 151638; PMID:96039533; PMID:7496627
A/Accession: 151638
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <ESP>
A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CA59679.1; PID:98546
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 88.0%; Score 81; DB 2; Length 790;
Best Local Similarity 83.3%; Pred. No. 0.0001;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTTVTTLTSDVNDNPP 18
||:||||:|||||
Db 248 AGTTTNTLTDVNDNPP 265

RESULT 5

152701
K-cadherin - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 152701
R:Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ottawara,
Cancer Res. 54, 3034-3041, 1994
A>Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer
A/Reference number: 152701; PMID:9423827; PMID:8187093
A/Accession: 152701
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-789 <RES>

A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435460
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185

Query Match 87.0%; Score 80; DB 2; Length 789;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTTVTTLTSDVNDNPP 18
||:||||:|||||
Db 249 SGTTLTTLTLDVNDNPP 266

RESULT 6

150178
cadherin-6B - chicken
C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: 150178
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe
A/Reference number: 150178; PMID:95309115; PMID:7540531
A/Accession: 150178
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <NA>
A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA07720.1; PID:986799
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTTVTTLTSDVNDNPP 18
||:||||:|||||
Db 249 SGTTLTTLTLDVNDNPP 266

RESULT 7

137016
cadherin-6 - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: 137016
R:Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S.
Cancer Res. 55, 2206-2211, 1995
A>Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the f
A/Reference number: 137016; PMID:95262134; PMID:7743525
A/Accession: 137016
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185

A/Cross-references: GDB:5822908
C/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-790 <RES>
A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185

Query Match 87.0%; Score 80; DB 2; Length 790;
Best Local Similarity 77.8%; Pred. No. 0.00015;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGTTVTTLTSDVNDNPP 18
||:||||:|||||
Db 249 SGTTLTTLTLDVNDNPP 266

RESULT 8

A38992
 Caderherin 11 precursor - human
 N/Alternate names: OB-cadherin, osteoblast
 C/Species: Homo sapiens (man)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: A38992
 R/Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
 A/Reference number: S24305; MUID:91283540; PMID:2059658
 A/Accession: A38992
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <SUZ>
 A/Cross-references: UNIPROT:P55287; GB:I34056; NID:9506403; PIDN:AAA35622.1; PID:9506404
 C/Genetics:
 A/Gene: GDB:CDH11; OB
 A/Cross-references: GDB:512891; OMIM:600023
 A/Map position: 16q22.1-16q22.1
 C/Superfamily: cadherin; cadherin repeat homology
 F/56-159/Domain: calcium binding; cell adhesion; duplication
 F/162-268/Domain: cadherin repeat homology <CR1>
 F/162-268/Domain: cadherin repeat homology <CR2>
 F/1271-383/Domain: cadherin repeat homology <CR3>
 F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
 ||:||||:|||||
 Db 249 SGTTKVTITLTDVNDNP 266

RESULT 9
 148277
 Caderherin-11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: 148277
 R/Hoffmann, I.; Belling, R.
 Dev. Biol. 169, 337-346, 1995
 A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
 A/Reference number: 148277; MUID:95269886; PMID:7750649
 A/Accession: 148277
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CAA54674.1; PID:96660
 C/Genetics:
 A/Gene: cad-11
 C/Superfamily: cadherin; cadherin repeat homology
 F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
 ||:||||:|||||
 Db 249 SGTTKVTITLTDVNDNP 266

RESULT 10
 149556
 Caderherin-11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: 149556
 R/Kimura, Y.; Matsumami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
 Dev. Biol. 169, 347-358, 1995
 A/Title: Cadherin-11 expressed in mesenchymal morphogenesis in the head

A/Reference number: 149556; MUID:95269887; PMID:7750650
 A/Accession: 149556
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; GB:D31963; NID:9974190; PIDN:BA06730.1; PID:997419
 F/56-159/Domain: cadherin repeat homology <CDH>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
 ||:||||:|||||
 Db 249 SGTTKVTITLTDVNDNP 266

RESULT 11
 A53584
 OB-cadherin precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C/Accession: A53584
 R/Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Amann, E.
 J. Biol. Chem. 269, 12092-12098, 1994
 A/Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
 A/Reference number: A53584; MUID:94216322; PMID:163513
 A/Accession: A53584
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-796 <OKA>
 A/Cross-references: UNIPROT:P55288; GB:D21253; NID:9994774; PIDN:BA04797.1; PID:999477
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: transmembrane protein
 F/56-159/Domain: cadherin repeat homology <CR1>
 F/162-268/Domain: cadherin repeat homology <CR2>
 F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 85.9%; Score 79; DB 2; Length 796;
 Best Local Similarity 77.8%; Pred. No. 0.00021;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTTVTLSDVNDNP 18
 ||:||||:|||||
 Db 249 SGTTKVTITLTDVNDNP 266

RESULT 12
 159372
 Caderherin 12 - human
 N/Alternate names: Br-cadherin
 C/Species: Homo sapiens (man)
 C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C/Accession: 159372
 R/Selley, S.; Bruno, S.; Schaff, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.I.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
 A/Title: Expressed cadherin pseudogenes are localized to the critical region of the spl
 A/Reference number: 159372; MUID:95249541; PMID:7731968
 A/Accession: 159372
 A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMI
 A/Molecule type: mRNA
 A/Residues: 1-794 <RES>
 A/Cross-references: UNIPROT:P55289; GB:I33477; NID:9793942; PIDN:AA848539.1; PID:979394;
 C/Genetics:
 A/Gene: GDB:CDH12
 A/Cross-references: GDB:596324
 A/Map position: 5p13-5p14
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
 F/57-160/Domain: cadherin repeat homology <CR1>
 F/163-269/Domain: cadherin repeat homology <CR2>
 F/272-384/Domain: cadherin repeat homology <CR3>

F:387-489/Domain: cadherin repeat homology <CR4>
 F:491-501/Domain: cadherin repeat homology <CR5>
 F:610-637/Domain: transmembrane #status predicted <TM>
 F:638-794/Domain: intracellular #status predicted <INT>

Query Match 77.2%; Score 71; DB 2; Length 794;
 Best Local Similarity 66.7%; Pred. No. 0.003;
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 SGGSTTVTLSDVNDNP 18
 DB 250 AGTTIVVTLTDVNDNP 267

RESULT 13

T30213
 G-cadherin - sea urchin (Lytechinus variegatus)
 C/Species: Lytechinus variegatus (variegated urchin)
 C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T30213
 R/Miller, J.R.; McClay, D.R.
 Dev. Biol. 192, 323-339, 1997
 A/Title: Characterization of the role of cadherin in regulating cell adhesion during sea
 A/Reference number: 220780; MUID:98104238; PMID:9441671
 A/Accession: T30213
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-2809 <ML>
 A/Cross-references: UNIPROT:O61230; EMBL:U34823; NID:92982186; PID:92982187; PIDN:AA0063

Query Match 72.8%; Score 67; DB 2; Length 2809;
 Best Local Similarity 66.7%; Pred. No. 0.068;
 Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SGGSTTVTLSDVNDNP 18
 DB 1694 SGATVAVTVTDVNDNP 1711

RESULT 14

T00252
 MEQFI protein - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C/Accession: T00252
 R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A/Reference number: 214126; MUID:98360089; PMID:9693030
 A/Accession: T00252
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-4351 <NA>
 A/Cross-references: UNIPROT:O88277; EMBL:AB011527; NID:93449285; PIDN:BAA32458.1; PID:93
 A/Experimental source: Brain
 C/Genetics:
 A/Gene: MEQFI
 C/Superfamily: rat MEQFI protein; cadherin repeat homology; EGF homology; laminin G repe
 F:3798-3949/Domain: laminin G repeat homology <LGR>
 F:3953-3985/Domain: EGF homology <EGF>
 F:3992-4023/Domain: EGF homology <EGF>

Query Match 70.7%; Score 65; DB 2; Length 4351;
 Best Local Similarity 61.1%; Pred. No. 0.23;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 SGGSTTVTLSDVNDNP 18
 DB 2360 TGETLVVNVSDINDNP 2377

RESULT 15

IOHUCS

cadherin 5 precursor - human
 N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1993 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: S49893; S24305; A43418
 R/Breviario, F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
 submitted to the EMBL Data Library, June 1994
 A/Description: Molecular and functional properties of VE-cadherin (784/cadherin-5) a nov
 A/Reference number: S49893

A/Accession: S49893
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-784

 A/Cross-references: UNIPROT:P3151; EMBL:X79981; NID:9599833; PIDN:CAA56306.1; PID:95998
 R/Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
 A/Reference number: S24305; MUID:91283540; PMID:2059658
 A/Accession: S24305
 A/Molecule type: mRNA
 A/Residues: 5-516; 'I', 518-784 <SUZ>
 A/Cross-references: EMBL:X59796; NID:9639976; PIDN:CAA42468.1; PID:929593
 R/Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Pisacane, A.; Huenen, G.; Rucco,
 J. Cell Biol. 118, 1511-1522, 1992
 A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts

A/Reference number: A43418; MUID:92394977; PMID:1522121
 A/Accession: A43418
 A/Molecule type: protein
 A/Residues: 48-60; 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-
 A/Experimental source: cultured endothelial cells
 A/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
 C/Genetics:
 A/Gene: GDB:CDH5
 A/Cross-references: GDB:134230; OMIM:601120

A/Map position: 16q22.1-16q22.1
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane prot
 F:1-25/Domain: signal sequence #status predicted <PRO>
 F:26-47/Domain: propeptide #status predicted <PRO>
 F:48-784/Product: cadherin 5 #status predicted <MAT>
 F:48-784/Domain: extracellular #status predicted <EXT>
 F:50-151/Domain: cadherin repeat homology <CR1>
 F:154-258/Domain: cadherin repeat homology <CR2>
 F:261-372/Domain: cadherin repeat homology <CR3>
 F:375-479/Domain: cadherin repeat homology <CR4>
 F:481-587/Domain: cadherin repeat homology <CR5>
 F:594-620/Domain: transmembrane #status predicted <TM>
 F:621-784/Domain: intracellular #status predicted <INT>
 F:736-753/Region: serine-rich
 F:61,112,157,362,442,523,535/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 67.4%; Score 62; DB 1; Length 784;
 Best Local Similarity 66.7%; Pred. No. 0.1;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 SGGSTTVTLSDVNDNP 18
 DB 239 SGATVAVTVTDVNDNP 256

Search completed: December 8, 2004, 10:27:08
 Job time: 2.45573 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 7.21488 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-12
Perfect score: 92
Sequence: 1 SGSTVTVTLSDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	92	100.0	Q86T00	Q86T00 homo sapien
2	92	100.0	Q96LQ7	Q96LQ7 homo sapien
3	92	100.0	Q6PFX6	Q6PFX6 mus musculu
4	92	100.0	AAH57373	AAH57373 mus muscu
5	92	100.0	CADO_HUMAN	CADO_HUMAN
6	92	100.0	Q8BLB5	Q8BLB5 mus musculu
7	92	100.0	Q6PANA	Q6PANA mus musculu
8	92	100.0	AAH60200	AAH60200 mus muscu
9	92	100.0	Q8C375	Q8C375 mus musculu
10	92	100.0	Q8C449	Q8C449 mus musculu
11	92	100.0	AAH57581	AAH57581 mus muscu
12	92	100.0	Q8BRK4	Q8BRK4 mus musculu
13	92	100.0	CADI_HUMAN	CADI_HUMAN
14	92	100.0	CAD8_HUMAN	CAD8_HUMAN
15	92	100.0	CAD8_MOUSE	CAD8_MOUSE
16	92	100.0	CAD8_RAT	CAD8_RAT
17	92	100.0	Q8BLT4	Q8BLT4 mus musculu
18	92	100.0	Q8AWM2	Q8AWM2 mus musculu
19	92	100.0	Q8IY78	Q8IY78 mus musculu
20	92	100.0	CAD7_CHICK	CAD7_CHICK
21	92	100.0	CAD7_HUMAN	CAD7_HUMAN
22	92	100.0	Q8BW92	Q8BW92 mus musculu
23	92	100.0	Q91838	Q91838 xenopus lae
24	92	100.0	CADA_HUMAN	CADA_HUMAN
25	92	100.0	Q8OWS7	Q8OWS7 mus musculu
26	92	100.0	Q8VI68	Q8VI68 mus musculu
27	92	100.0	AAH62962	AAH62962 mus muscu
28	92	100.0	CAD6_RAT	CAD6_RAT
29	92	100.0	CADA_CHICK	CADA_CHICK
30	92	100.0	CAD6_CHICK	CAD6_CHICK
31	92	100.0	CAD6_HUMAN	CAD6_HUMAN

32	80	87.0	790	1	CAD6_MOUSE	P97326 mus musculu
33	80	87.0	798	2	Q7ZYV7	Q7ZYV7 gallus gall
34	80	87.0	798	2	Q8GGH3	Q8GGH3 gallus gall
35	80	87.0	801	1	CADK_HUMAN	Q9DHC6 homo sapien
36	80	87.0	801	2	Q9ZOM3	Q9ZOM3 mus musculu
37	80	87.0	813	1	CADM_MOUSE	Q9WTP5 mus musculu
38	80	87.0	813	1	CADM_RAT	Q63315 ratcus norv
39	80	87.0	828	1	CADM_HUMAN	Q9UJ99 homo sapien
40	79	85.9	792	1	CAD8_CHICK	Q93319 gallus gall
41	79	85.9	794	2	O93264	O93264 xenopus lae
42	79	85.9	796	1	CADB_HUMAN	P55287 homo sapien
43	79	85.9	796	1	CADB_MOUSE	P55288 mus musculu
44	79	85.9	796	2	Q8C706	Q8C706 mus musculu
45	75	81.5	789	1	CAD9_HUMAN	Q9UBD4 homo sapien

ALIGNMENTS

RESULT 1	Q86T00	PRELIMINARY;	PRT;	370 AA.
AC	Q86T00;			
DT	01-JUN-2003 (TREMBlrel. 24, Created)			
DT	01-JUN-2003 (TREMBlrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Full-length cDNA clone CS0DX003Y017 of Hela cells of Homo sapiens (human) (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hela cells;			
RA	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hela cells;			
RA	Genoscope;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Contains 4 cadherin domains.			
DR	EMBL; BX248303; CAD62530.1;			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.			
DR	InterPro; IPR02126; Cadherin.			
DR	Pfam; PF00028; Cadherin; 3.			
DR	PRINTS; PR00205; CADHERIN.			
DR	SMART; SMO0112; CA_2.			
DR	PROSITE; PS00232; CADHERIN_1; 1.			
DR	PROSITE; PS50268; CADHERIN_2; 4.			
KW	Calcium; Calcium-binding.			
FT	NON_TER 1			
FT	NON_TER 370			
SQ	SEQUENCE 370 AA; 39479 MW; 3996D4AF8A4500E0 CRC64;			
Query Match	100.0%; Score 92; DB 2; Length 370;			
Best local Similarity	100.0%; Pred. No. 4.7e-06;			
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Cy	1 SGSTVTVTLSDVNDNP 18			
Db	1 SGSTVTVTLSDVNDNP 18			
RESULT 2	Q96LQ7	PRELIMINARY;	PRT;	493 AA.
ID	Q96LQ7			
AC	Q96LQ7;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			

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DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein FLJ25193.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Nimmiya K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Nakatani N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 cadherin domains.
DR EMBL: AK057922; BAB71613.1;
DR HSSP: P12830; 1065.
DR Genew: HGNC:14265; CDH24.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:phospholipid cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR Pfam: PF00028; Cadherin; 4.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 4.
DR PROSITE: PS00232; CADHERIN_1; 2.
DR PROSITE: PS00268; CADHERIN_2; 4.
KW Calcium; Calcium-binding;
SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;

Query Match 100.0%; Score 92; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 6,5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 240 SGGTIVTVTLSDVNDNPP 257

ID |||||
AC AAH57373 PRELIMINARY; PRT; 781 AA.
ID O6PFK6
AC O6PFK6 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Cadherin-like 24.
GN Name=CDH24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Richards S., Worley K.C., Harte S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: BC057373; AAH57373.1;
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin; 1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 4.
DR PROSITE: PS00232; CADHERIN_1; 2.
DR PROSITE: PS00268; CADHERIN_2; 5.
KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835AA CRC64;

Query Match 100.0%; Score 92; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 240 SGGTIVTVTLSDVNDNPP 257

ID |||||
AC AAH57373 PRELIMINARY; PRT; 781 AA.
ID AAH57373;
AC AAH57373 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Cadherin-like 24.
GN CDH24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Richards S., Worley K.C., Harte S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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RP SEQUENCE FROM N.A. TISSUE=Brain;
RC STRAIN=C57BL/6;
RA Strauberg R.;
RL Submitted (Sep-2003) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 781 AA; 84104 MW; 15996D6EC9835AA CRC64;
Query Match: 100.0%; Score 92; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSGTIVTVTLSDVANDNP 18
Db 240 GSGTIVTVTLSDVANDNP 257
RESULT 5
ID CADO_HUMAN STANDARD: PRT, 819 AA.
CA CADO_HUMAN
AC Q86UP0; Q86UP1; Q9NT84;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ2834/PRO34009).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP CATEININS.
RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RX Katsifiasz B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
RT II cadherin".
RL J. Biol. Chem. 278:27513-27519(2003).
[2]
RN
RP SEQUENCE FROM N.A. (ISOFORM 2)
RX MEDLINE=22687296; PubMed=12975309; DOI=10.1101/gr.1293003;
RX Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Batson D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh U., Smith V., Stinson J., Vagts A.,
RA Vanlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment".
RL Genome Res. 13:12265-2270(2003).
[3]
RN
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Testis;
RA Blum H., Baerachar S., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ database.
-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
They preferentially interact with themselves in a homophilic
manner in connecting cells; cadherins may thus contribute to the
sorting of heterogeneous cell types. Cadherin-24 mediate strong
cell-cell adhesion.
-1- SUMMARY: Associates with alpha-, beta- and delta-catenins.
-1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1; Synonyms=Long form;
IsoId=Q86UP0-1; Sequence=1isplayed;
Name=2; Synonyms=Short form;
IsoId=Q86UP0-2; Sequence=VSP_008717;
Name=3;
IsoId=Q86UP0-3; Sequence=VSP_008718, VSP_008719;
CC

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CC CC Note=No experimental confirmation available;
CC CC -I- SIMILARITY: Contains 5 cadherin domains.
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CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
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CC CC or send an email to license@isb-sib.ch).
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CC CC -----
CC DR EMBL/ AY260590; AAP20590.1; --
CC DR EMBL/ AY260591; AAP20591.1; --
CC DR EMBL/ AY358199; AAQ88566.1; --
CC DR EMBL/ AL137477; CAB70758.1; --
CC DR PIR; T46418; T46418.
CC DR HSSP; P09803; I17W.
CC DR Genew; HGNC:14265; CDH24.
CC DR InterPro; IPR002126; Cadherin_C_term.
CC DR InterPro; IPR002033; Cadherin_C_term.
CC DR Pfam; PF00208; Cadherin; 5.
CC DR Pfam; PF01049; Cadherin_C_1.
CC DR PRINTS; PR00235; CADHERIN.
CC DR PROSITE; PS00232; CADHERIN_1; 2.
CC DR PROSITE; PS00268; CADHERIN_2; 5.
CC KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
CC MW Multigene family; Repeat; Signal; Transmembrane.
CC FT SIGNAL 1 19 Potential.
CC FT PROPEP 21 44 Potential.
CC FT CHAIN 45 819 Cadherin-24.
CC FT DOMAIN 45 641 Extracellular (Potential).
CC FT TRANSHEM 642 662 Potential.
CC FT DOMAIN 663 819 Cytoplasmic (Potential).
CC FT DOMAIN 46 150 Cadherin 1.
CC FT DOMAIN 151 259 Cadherin 2.
CC FT DOMAIN 260 374 Cadherin 3.
CC FT DOMAIN 375 517 Cadherin 4.
CC FT DOMAIN 517 630 Cadherin 5.
CC FT CARBOHYD 446 446 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 548 548 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 563 563 N-linked (GlcNAc...) (Potential).
CC FT VASPLIC 455 492 Missing (in isoform 2).
CC FT VASPLIC 455 492 /FtId=VSP_008717.
CC FT VASPLIC 1 427 Missing (in isoform 3).
CC FT VASPLIC 1 427 /FtId=VSP_008718.
CC FT VASPLIC 428 492 ECTHTTAFLDRERAMNLT/LATELGMSGPERGYBL
CC FT VASPLIC 428 492 VAEMSAAPAPQRPSUGAVGIPO -> MNIVCTWYCSHS
CC FT VASPLIC 428 492 ALTFSTGLHAIFMCFGLMYLASGGIHAAHPMLRVNVCYC
CC FT VASPLIC 428 492 VMRVCFGLVLPs (in isoform 3).
CC FT VASPLIC 428 492 /FtId=VSP_008719.
CC SQ SEQUENCE 819 AA; 87751 MM; 9083034FI8BA7EA4 CRC64;
CC QY Query Match 100.0%; Score 92; DB 1; Length 819;
CC Db Best Local Similarity 100.0%; Pred. NO. 1.le-05; Indels 0; Gaps 0
CC Matches 18; Conservative 0; Mismatches 0;
CC 1 SGSTVTVTLSVDNDNP 18
CC ||| ||||| ||||| |||||
CC 240 SGSTVTVTLSVDNDNP 257
CC RESULT 6
CC QBIBLS PRELIMINARY; PRT; 337 AA.
CC ID QBIBLS;
CC AC 01-MAR-2003 (TREMBLrel. 23. Created)
CC DT 01-MAR-2003 (TREMBLrel. 23. Last sequence update)
CC DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)
CC DE Mus musculus adult male corpora quadrigena cDNA, RIKEN full-length
CC enriched library, clone:B230220E17 product:hypothetical cadherin
CC structure containing protein, full insert sequence. (Fragment).
CC GN Name=B230220B17Rik;
CC OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076851;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Boro H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nihei K., Nomura K., Numazaki R., Ohno M., Obatao N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1. SIMILARITY: Contains 3 cadherin domains.
DR EMBL; AK045672; BAC32451.1; -
DR HSSP; P15116; INCT
DR MGD; MGI:2444914; B23020201791K.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; Cadherin.3.
DR PRINTS; PR00205; CADHERIN.

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DR SMART; SM00112; CA_2
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 3.
KW Calcium; Calcium-binding; Hypothetical protein.
FT NON TER 337
SQ SEQUENCE 337 AA; 37137 MW; C81B98A3038FA10C CRC64;
Query Match 90.2%; Score 83; DB 2; Length 337;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGGSTVTVTLSDVNDNPP 18
Db 249 SGGSTVTNITLTVDNDNPP 266
RESULT 7
ID O6PAN4 PRELIMINARY; PRT; 508 AA.
AC O6PAN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Strausberg R.;
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1. SIMILARITY: Contains 4 cadherin domains.
DR EMBL; BC060200; AAH60200.1; -
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; Cadherin.4.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA_4
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 4.
DR KEGG; K04600; Calcium-binding.
DR KEGG; K04600; Calcium-binding.
SQ SEQUENCE 508 AA; 56388 MW; 9053F774BCE52255 CRC64;
Query Match 90.2%; Score 83; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTVTVTLSDVNDNPP 18

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DB      257  SGTTLVT/LT/DVNDNPP 274
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RESULT 8
AAH60200 PRELIMINARY; PRT; 508 AA.
ID      AAH60200;
AC      AAH60200;
DT      02-MAR-2004 (TREMBlrel. 27, Created)
DT      02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT      02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE      Cdh8 protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RC      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stalcleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA      Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Paney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA      Kravitz M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Merra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RT      [Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).]
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RC      Strausberg R.;
RL      Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
DR      EMBL; BC060200; AAH60200.1;
SQ      SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;

Query Match      90.2%; Score 83; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 0.00018;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTIVT/LTSPVNDNPP 18
DB      257  SGTTLVT/LT/DVNDNPP 274
      |||:|||||:|||||
ID      08C375 PRELIMINARY; PRT; 716 AA.
AC      08C375;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DE      library, clone:ID30046N17 Product:cadherin 8, full insert
DE      sequence.
GN      Name=Cdh8;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]

RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RX      MEDLINE=99279253; PubMed=10349636;
RA      Carninci P., Hayashizaki Y.;
RT      "High-efficiency full-length cDNA cloning."
RL      Meth. Enzymol. 303:19-44 (1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RX      MEDLINE=21085660; PubMed=11217851;
RA      RIKEN FANTOM Consortium;
RT      "Functional annotation of a full-length mouse cDNA collection."
RL      Nature 409:685-690 (2001).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RA      The FANTOM Consortium;
RT      "Analysis of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs."
RL      Nature 420:563-573 (2002).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RC      MEDLINE=2049374; PubMed=11042159;
RA      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA      Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT      "Normalization and substructure of cap-trapper-selected cDNAs to
RT      prepare full-length cDNA libraries for rapid discovery of new genes."
RL      Genome Res. 10:1617-1630 (2000).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RC      MEDLINE=20530913; PubMed=11076861;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA      Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA      Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA      Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA      Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA      Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Muramatsu S., Kawai J.,
RA      Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT      "RIKEN integrated sequence analysis (RISA) system-384-format
RT      sequencing pipeline with 384 multiloop capillary sequencer."
RL      Genome Res. 10:1757-1771 (2000).
RN      [6]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
RA      Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA      Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA      Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA      Hori F., Imochi K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA      Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA      Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura Y.,
RA      Nishi K., Nomura K., Numaaki R., Ohno M., Ohsato N., Okazaki Y.,
RA      Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA      Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA      Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA      Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT      Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
RN      [7]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Head;
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC      -1- SIMILARITY: Contains 5 cadherin domains.
DR      EMBL; AK086711; BAC39724.1;
DR      HESP; P1516; INCU.
DR      MGD; MGI:107434; Cdh8.
DR      GO; GO:0016020; C=membrane; IEA.
DR      GO; GO:0005509; F=calcium ion binding; IEA.
DR      GO; GO:0007156; P=homophilic cell adhesion; IEA.
DR      InterPro; IPR002126; Cadherin.
DR      InterPro; IPR002333; Cadherin_C-term.
DR      Pfam; PF00028; Cadherin; 5.
DR      Pfam; PF01049; Cadherin_C; 1.

```


DB 257 GCTTTLVTLVDVNDNP 274

RESULT 11

AAH57581 PRELIMINARY; PRT; 716 AA.

01-MAR-2004 (TREMBlrel. 27, Created)

02-MAR-2004 (TREMBlrel. 27, Last sequence update)

02-MAR-2004 (TREMBlrel. 27, Last annotation update)

03 Mus musculus (Mouse).

04 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

05 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

06 NCB1_taxid=10090;

07 SEQUENCE FROM N.A.

08 STRAIN=C57BL/6; TISSUE=Brain;

09 MEDLINE=22388257; PubMed=12477932;

10 Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

11 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

12 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

13 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

14 Stralson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

15 Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,

16 Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

17 Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

18 Villalón D.K., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,

19 Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

20 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

21 Blakesley A.C., Grimwood J., Schmutz J., Dickson M.C.,

22 Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,

23 Jones S.J., Marra M.A.,

24 "Generation and initial analysis of more than 15,000 full-length human

25 and mouse cDNA sequences.";

26 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

27 [2]

28 SEQUENCE FROM N.A.

29 STRAIN=C57BL/6; TISSUE=Brain;

30 Strausberg R.,

31 Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

32 EMBL; BC057581; AAH57581.1;

33 SEQUENCE 716 AA; 79145 MW; 976FF5D845F938D CRC64;

34 Query Match 90.2%; Score 83; DB 2; Length 716;

35 Best Local Similarity 83.3%; Pred. No. 0.00026; Indels 0; Gaps 0;

RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.,

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44 (1999).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;

RD MEDLINE=21085660; PubMed=11217851;

RE RIKEN PANTOM Consortium;

RF "Functional annotation of a full-length mouse cDNA collection.";

RG Nature 409:685-690 (2001).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;

RD The PANTOM Consortium;

RE the RIKEN Genome Exploration Research Group Phase I & II Team;

RF "Analysis of the mouse transcriptome based on functional annotation of

RG 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;

RD MEDLINE=20499374; PubMed=11042159;

RE Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RF Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,

RG "Normalization and subtraction of cap-trapper-selected cDNAs to

RH prepare full-length cDNA libraries for rapid discovery of new genes.";

RI Genome Res. 10:1617-1630 (2000).

[5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;

RD MEDLINE=2050913; PubMed=11076861;

RE Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RF Kono H., Akiyama J., Nishi K., Katsunai T., Taishiro H., Itoh M.,

RG Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,

RH Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashigaki M.,

RI Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,

RJ Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,

OKazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RT "RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multichannel sequencer.";

RI Genome Res. 10:1757-1771 (2000).

[6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;

RD Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RE Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RF Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RG Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RI Karch H., Kawai J., Kojima Y., Kondo S., Kono H., Koyama M., Koya S.,

RJ Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RS Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

RT Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RU Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RV Tagawa A., Takahashi F., Takaku-Akita S., Takekura Y., Tanaka T.,

RW Tomaru A., Toya T., Yasunishi A., Yamamoto M., Hayashizaki Y.,

RY Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

[7]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cortex;

RD -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).

RE -1- SIMILARITY: Contains 5 cadherin domains.

RF EMBL; AK044046; BAC11751.1; -

RG HSSP; P15116; INCU.

RI GO; GO:0016020; C:membrane; IEA.

RS GO; GO:0005509; F:calcium ion binding; IEA.

RT GO; GO:0007156; P:homophilic cell adhesion; IEA.

RV InterPro; IPR002126; Cadherin.

RY InterPro; IPR002333; Cadherin_C-term.

ZZ Pfam; PF00028; Cadherin; 5.

ZZ Pfam; PF01043; Cadherin_C_1.

ZZ PRINTS; PR00205; CADHERIN.

ZZ SMART; SM00112; CA; 5.

ZZ PROSITE; PS00232; CADHERIN_1; 3.

DR PROSITE; PS50268; CADHERIN 2; 5.
 KM Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 754 AA, 83624 MW, 149C3C70D3F21568 CRC64.

Query Match 90.2%; Score 83; DB 2; Length 754;
 Best Local Similarity 83.3%; Pred. No. 0.00028;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTWTVTLSVDNDNP 18
 |||:||||:|||||
 Db 257 SGTTLTITLTDVNDNP 274

RESULT 13
 CADI_HUMAN STANDARD; PRT; 790 AA.
 AC Q13634;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Cadherin-18 precursor (Cadherin-14).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97184182; PubMed=9030594;
 RA Shibata T., Shimoyama Y., Gotoh M., Hirohashi S.;
 RT "Identification of human cadherin-14, a novel neurally specific type
 II cadherin, by protein interaction cloning."
 RL J. Biol. Chem. 272:5236-5240(1997).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC
 CC EMBL; U59325; AAB02933.1; -
 CC PIR; G02678; G02678.
 CC HSSD; P09803; 117X.
 CC Genew; HGNC:1757; CDH18.
 CC MIM; 603019; -
 CC InterPro; IPR002126; Cadherin.
 CC InterPro; IPR000233; Cadherin_C-term.
 CC Pfam; PF00028; Cadherin_5.
 CC Pfam; PF01049; Cadherin_C_1.
 CC PRINTS; PR00205; CADHERIN.
 CC SMART; SM00112; CA_5.
 CC PROSITE; PS00232; CADHERIN_1; 3.
 CC PROSITE; PS50268; CADHERIN_2; 5.
 KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 790 Cadherin-18.
 FT DOMAIN 54 608 Extracellular (Potential).
 FT TRANSMEM 609 636 Potential.
 FT DOMAIN 637 790 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.

FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 36 36 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 255 255 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 790 AA, 88072 MW, 5C7BDEB229B6EDCA CRC64;

Query Match 90.2%; Score 83; DB 1; Length 790;
 Best Local Similarity 83.3%; Pred. No. 0.0003;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTWTVTLSVDNDNP 18
 |||:||||:|||||
 Db 249 SGTTLTITLTDVNDNP 266

RESULT 14
 CADI_HUMAN STANDARD; PRT; 799 AA.
 ID CAD8_HUMAN
 AC P5286; Q9UBH2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitejima M., Natori M.;
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins."
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins classifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin."
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Retal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue."
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
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 CC

EMBL; AB035305; BA07419.1; -
 DR EMBL; U34060; AAA35628.1; ALT_INIT.
 DR HSP; P09803; 117W.
 DR Genew; HGNC:1767; CDH8.
 DR MIM; 603008; -.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 Transmembrane.
 KW SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 799 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 643 799 Cadherin 1.
 FT DOMAIN 643 799 Cadherin 2.
 FT DOMAIN 643 799 Cadherin 3.
 FT DOMAIN 643 799 Cadherin 4.
 FT DOMAIN 643 799 Cadherin 5.
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 355 355 V -> D (in Ref. 2 and 3).
 FT CONFLICT 647 647 H -> HO (in Ref. 2 and 3).
 FT SEQUENCE 799 AA; 88253 MW; 9819886039C640A CR64;
 SQ
 Query Match 90.2%; Score 83; DB 1; Length 799;
 Best Local Similarity 83.3%; Pred. No. 0.0003;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTTVTTLSPVNDNP 18
 DB 257 SGTTLVTTLVDVNDNP 274
 RESULT 15
 CAR8_MOUSE STANDARD; PRT; 799 AA.
 ID CAD8_MOUSE
 AC P97291;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX MEDLINE=97174321; PubMed=5022055;
 RA Kurematu K., Redies C.;
 RT "Restricted expression of cadherin-8 in segmental and functional
 subdivisions of the embryonic mouse brain.";
 RL Dev. Dyn. 208:178-189(1997).
 CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 5 cadherin domains.

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 DR EMBL; X95600; CA64857.1; -
 DR HSP; P09803; 117W.
 DR MGD; MGI:107434; Cdh8.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 Transmembrane.
 KW SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 799 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 643 799 Cadherin 1.
 FT DOMAIN 643 799 Cadherin 2.
 FT DOMAIN 643 799 Cadherin 3.
 FT DOMAIN 643 799 Cadherin 4.
 FT DOMAIN 643 799 Cadherin 5.
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CR64;
 SQ
 Query Match 90.2%; Score 83; DB 1; Length 799;
 Best Local Similarity 83.3%; Pred. No. 0.0003;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTTVTTLSPVNDNP 18
 DB 257 SGTTLVTTLVDVNDNP 274
 Search completed: December 8, 2004, 10:24:39
 Job time : 7.21488 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 (Search time 7.44864 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-12

Perfect score: 92
Sequence: 1 SGSTTVTVTLSDVNDNPP 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20048:*

8: Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	18	7	ADD29453 Human cad
2	92	100.0	18	7	ADD29452 Human cad
3	92	100.0	493	5	AD116946 Human NOV
4	92	100.0	607	5	ABBS3295 Human NOV
5	92	100.0	620	7	ADD29448 Human cad
6	92	100.0	636	7	ADD29445 Human cad
7	92	100.0	781	5	ABBS3296 Human pol
8	92	100.0	781	5	AAW48735 Human cad
9	92	100.0	781	5	ABG34078 Human pro
10	92	100.0	781	5	AD116604 Human NOV
11	92	100.0	781	5	AD116606 Human NOV
12	92	100.0	781	6	ABR40114 Human cel
13	92	100.0	781	6	ADA01366 Human PRO
14	92	100.0	781	6	ADA43795 Human sec
15	92	100.0	781	6	ADA43563 Human sec
16	92	100.0	781	6	ADA01238 Human PRO
17	92	100.0	781	7	ADA01122 Human sec
18	92	100.0	781	7	ADA01367 Human sec
19	92	100.0	781	7	ADA06941 Human PRO
20	92	100.0	781	7	ADA08429 Human hum
21	92	100.0	781	7	ADBS9722 Human PRO
22	92	100.0	781	7	ADBS87005 Human PRO
23	92	100.0	781	7	ADBS65160 Human sec
24	92	100.0	781	7	ADBS9858 Human PRO
25	92	100.0	781	7	ADBS99493 Human hum

26	92	100.0	781	7	ADB66044 Human sec
27	92	100.0	781	7	ADC23442 Human tra
28	92	100.0	781	7	ADC26135 Human PRO
29	92	100.0	781	7	ADG04962 Human PRO
30	92	100.0	781	7	ADG11268 Human PRO
31	92	100.0	781	7	ADG88199 Human PRO
32	92	100.0	781	7	ADG95494 Human sec
33	92	100.0	781	7	ADG06424 Human PRO
34	92	100.0	781	7	ADG38199 Human PRO
35	92	100.0	781	7	ADG88315 Human PRO
36	92	100.0	781	7	ADG90896 Human sec
37	92	100.0	781	7	ADG99451 Human PRO
38	92	100.0	781	7	ADG06544 Human PRO
39	92	100.0	781	7	ADG05495 Human PRO
40	92	100.0	781	7	ADG82496 Human PRO
41	92	100.0	781	8	ADG51749 Human sec
42	92	100.0	781	8	ADG51965 Human sec
43	92	100.0	781	8	ADG37723 Human sec
44	92	100.0	781	8	ADG37607 Human sec
45	92	100.0	781	8	ADG95378 Human sec

ALIGNMENTS

RESULT 1
ADD29453
ID ADD29453 standard; peptide; 18 AA.
XX
AC ADD29453:
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like protein peptide fragment Seq ID12.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytoskeletal; osteopetrosis; cancer;
KW osteopetrosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US200314491-A1.
XX
FD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (GDB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LITC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
PI Liu C, Drmanac RT;
XX
WR: 2003-829799/77.
XX
PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteopetrosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX
PS Claim 11; SEQ ID NO 12; 63bp; English.
CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, CC hyperostosis and osteopetrosis. The protein and DNA sequence of the CC invention may also be useful as markers for prognosis of metastatic CC tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA;

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
Db 1 SGGTIVTVTLSDVNDNPP 18

RESULT 2
ADD29452
ID ADD29452 standard; peptide; 18 AA.

AC ADD29452;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein peptide fragment Seq ID11.

XX cadherin-like protein; transmembrane protein; cadherin domain;

XX homotypic cell-cell adhesion; cytostatic; osteopathic; cancer;

XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;

XX metastatic tumour; human.

OS Homo sapiens.

PN US2003144491-A1.

XX 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

XX (GDB/) GODBOLE S D.

PA (KDOC/) KOC C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;

PI Liu C, Drmanac RT;

DR WPI, 2003-823799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 11; 63bp; English.

cell adhesion that is calcium dependent. Modulators of the protein of the CC invention may have cytostatic or osteopathic activity. The invention may CC allow development of therapeutics useful for the treatment of diseases CC such as cancers, osteoporosis, Paget's disease, osteomalacia, CC hyperostosis and osteopetrosis. The protein and DNA sequence of the CC invention may also be useful as markers for prognosis of metastatic CC tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

Sequence 18 AA;

Query Match 100.0%; Score 92; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTIVTVTLSDVNDNPP 18
Db 1 SGGTIVTVTLSDVNDNPP 18

RESULT 3
AD116946
ID AD116946 standard; protein; 493 AA.

AC AD116946;

DT 15-APR-2004 (first entry)

DE Human NOVX protein homologue SeqID 482.

XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

XX inflammation; autoimmune disorder; allergy; blood disorder;

XX acquired immunodeficiency syndrome; AIDS; obesity; asthma;

XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;

XX Alzheimer's disease; infection; str.

OS Homo sapiens.

PN WO200268649-A2.

XX 06-SEP-2002.

PF 31-JAN-2002; 2002WO-US002785.

PR 31-JAN-2001; 2001US-0265395P.

PR 31-JAN-2001; 2001US-0265412P.

PR 31-JAN-2001; 2001US-0265514P.

PR 31-JAN-2001; 2001US-0265517P.

PR 02-FEB-2001; 2001US-0266406P.

PR 05-FEB-2001; 2001US-0266767P.

PR 07-FEB-2001; 2001US-0266975P.

PR 08-FEB-2001; 2001US-0267057P.

PR 09-FEB-2001; 2001US-0267459P.

PR 15-FEB-2001; 2001US-0268974P.

PR 26-FEB-2001; 2001US-0271664P.

PR 27-FEB-2001; 2001US-0271839P.

PR 02-MAR-2001; 2001US-0271855P.

PR 14-MAR-2001; 2001US-0272788P.

PR 02-MAR-2001; 2001US-0273046P.

PR 14-MAR-2001; 2001US-0273925P.

PR 14-MAR-2001; 2001US-0275950P.

PR 14-MAR-2001; 2001US-0275989P.

PR 15-MAR-2001; 2001US-0276448P.

PR 15-MAR-2001; 2001US-0276450P.

PR 16-MAR-2001; 2001US-0276397P.

PR 16-MAR-2001; 2001US-0276768P.

PR 20-MAR-2001; 2001US-0278652P.

PR 26-MAR-2001; 2001US-0278775P.

PR 26-MAR-2001; 2001US-0278778P.

PR 29-MAR-2001; 2001US-0279882P.

Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
|||||
Db 240 SGGTIVTTLSDVNDNPP 257

RESULT 4
ABBS3295
ID ABBS3295 standard; protein; 607 AA.
AC ABBS3295;
XX

DT 12-FEB-2002 (first entry)
XX

DE Human polypeptide #35.
XX

Human; neurotropic; neuroprotective; anticonvulsant; antidepressant;
KW neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
KW antiinflammatory; antidiabetic; hepatotropic; virucide; antidiabetic;
KW nephrotropic; anorectic; cyrostatic; vaccine; neurological disease;
KW cardiovascular disease; respiratory disease; liver disease;
KW renal disease; skeletal muscle disease; gastrointestinal disease;
KW placental disease; testicular cancer; male fertility; pancreatic disease.
XX

OS Homo sapiens.
XX

PN W0200181363-A1.
XX

PD 01-NOV-2001.
XX

PF 26-APR-2001; 2001WO-US013360.
XX

PR 27-APR-2000; 2000US-0199963P.
PR 11-MAY-2000; 2000US-0203336P.
PR 25-MAY-2000; 2000US-0207087P.
PR 26-MAY-2000; 2000US-0207546P.
XX

PA (SMIK) SMITHKLINE BEECHAM CORP.
PI (SMIK) SMITHKLINE BEECHAM PLC.
XX

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kahnack KS;
PI Lai Y, Xie Q;
XX

DR WPI: 2002-041392/05.
DR N-PSDB; ABA90360.
XX

PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
PT and treating diseases associated with the polypeptide, e.g. Alzheimer's
PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
XX

PS Claim 1; Page 106-108; 116pp; English.
XX

XX The invention relates to an isolated polypeptide comprising a 277, 480,
CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
CC 844, 782, 262, 394, 471, 485, 266, 533, 495, 350, 619, 490, 462, 255,
CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
CC given in the specification. The polypeptides, modulators of the
CC polypeptides and antibodies against the polypeptides are useful for
CC treating diseases such as neurological and psychiatric diseases including
CC Alzheimer's, parasympathetic palsy, Huntington's disease, myotonic
CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle disease including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymph diseases including

PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285745P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312885P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318118P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CUBA-) CUBAGEN CORP.
XX
XX Tchernev VT, Spytek KA, Zerkusen BD, Patrujan M, Shinkets RA;
PI Li L, Gangolli EA, Padigaru M, Anderson DM, Pastelli L, Miller CE;
PI Gerlach VL, Taupier RJ, Gusev YV, Colman SD, Wolenc AR, Pena CE;
PI Furrak K, Grose WM, Alsdbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI: 2002-706998/76.
DR
XX
XX New NOXV polypeptides and nucleic acids, useful for preventing or
PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure; SEQ ID NO 482; 1498pp; English.
XX
XX This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC disease pathological conditions. The present invention describes novel
CC human and murine NOXV proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOXV polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cyrostatic, cardiac antiinflammatory, immunosuppressive, anti-allergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antisthmatic, neurotropic, antiarrhythmic, hepatotropic,
CC neuroprotective, neurotropic, antibacterial, virucide, antidiabetic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
CC of the invention.
XX
XX Sequence 493 AA;

CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility, and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX
SQ Sequence 607 AA;

Query Match 100.0%; Score 92; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
Db 240 SGSTVTVTLSDVNDNPP 257

RESULT 5
ADD29448
ID ADD29448 standard; protein; 620 AA.

AC ADD29448;
XX
XX

DT 15-JAN-2004 (first entry)
XX

DE Human cadherin-like mature protein.
XX

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.
XX

OS Homo sapiens.
XX

PN US2003144491-A1.
XX

PD 31-JUL-2003.
XX

PF 16-FEB-2001; 2001US-00788051.
XX

PR 03-FEB-2000; 2000US-00496914.
XX

PR 27-APR-2000; 2000US-00560875.
XX

PA (GODB/) GODBOLE S D.
XX

PA (KUOC/) KUO C.
XX

PA (ARTE/) ARTERBURN M C.
XX

PA (YEUN/) YEUNG G.
XX

PA (PALE/) PALENCIA S.
XX

PA (TANG/) TANG Y T.
XX

PA (LIUC/) LIU C.
XX

PA (DRMA/) DRMANAC R T.
XX

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
XX

PI Liu C, Drmanac RT;
XX

DR WPI; 2003-829799/77.
XX

PS Claim 11; SEQ ID NO 7; 63pp; English.
XX

This invention relates to a novel isolated human secreted cadherin-like protein and the DNA sequence which encodes it. Cadherins are a family of transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may allow development of therapeutic useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of the mature human secreted

CC cadherin-like protein which was used during the exemplification of the
CC invention.
XX
SQ Sequence 620 AA;

Query Match 100.0%; Score 92; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTVTVTLSDVNDNPP 18
Db 224 SGSTVTVTLSDVNDNPP 241

RESULT 6
ADD29445
ID ADD29445 standard; protein; 636 AA.

AC ADD29445;
XX

DT 15-JAN-2004 (first entry)
XX

DE Human cadherin-like protein amino acid sequence.
XX

XX cadherin-like protein; transmembrane protein; cadherin domain;
XX homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
XX osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
XX metastatic tumour; human.
XX

OS Homo sapiens.
XX

FN Key Location/Qualifiers
XX

FT Peptide 1..16
XX

FT Protein /label=Signal_peptide
XX

FT /label=Mature_human_cadherin-like_protein
XX

PN US2003144491-A1.
XX

PD 31-JUL-2003.
XX

PF 16-FEB-2001; 2001US-00788051.
XX

PR 03-FEB-2000; 2000US-00496914.
XX

PR 27-APR-2000; 2000US-00560875.
XX

PA (GODB/) GODBOLE S D.
XX

PA (KUOC/) KUO C.
XX

PA (ARTE/) ARTERBURN M C.
XX

PA (YEUN/) YEUNG G.
XX

PA (PALE/) PALENCIA S.
XX

PA (TANG/) TANG Y T.
XX

PA (LIUC/) LIU C.
XX

PA (DRMA/) DRMANAC R T.
XX

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;
XX

PI Liu C, Drmanac RT;
XX

DR WPI; 2003-829799/77.
XX

PS Claim 11; SEQ ID NO 4; 63pp; English.
XX

This invention relates to a novel isolated human secreted cadherin-like protein and the DNA sequence which encodes it. Cadherins are a family of transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutics useful for the treatment of diseases
CC such as cancer, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

XX Sequence 636 AA;

Query Match 100.0%; Score 92; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
Db 240 SGGTTVTVTLSDVNDNPP 257

RESULT 7
ABBS3296
ID ABBS3296 standard; protein; 781 AA.

XX ABBS3296;

DT 12-FEB-2002 (first entry)

XX Human polypeptide #36.

XX Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; antiarrhythmic; cardiant; antidiabetic;
XX antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
XX nephrotropic; anorectic; cyclostatic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

XX WO200181363-A1.

XX 01-NOV-2001.

XX 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

XX 11-MAY-2000; 2000US-0203336P.

XX 25-MAY-2000; 2000US-0207087P.

XX 26-MAY-2000; 2000US-0207546P.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX (SMK) SMITHKLINE BEECHAM PLC.

XX Aggarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;

XX Lai Y, Xie Q;

XX WPI: 2002-041392/05.

XX N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing

XX disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

XX Claim 1; Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,

XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,

XX 844, 782, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,

XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as

XX given in the specification. The polypeptides, modulators of the

XX polypeptides and antibodies against the polypeptides are useful for

XX treating diseases such as neurological and psychiatric diseases including

XX Alzheimer's, paraproteinemia, Huntington's disease, myotonic

XX dystrophy, anorexia and depression; cardiovascular diseases including

CC congestive heart failure, Hodgkin's disease and myocardial infarction;

CC respiratory diseases including asthma, chronic obstructive pulmonary

CC disease, cystic fibrosis and adult respiratory distress syndrome; liver

CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral

CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;

CC renal disease including renal failure, acute tubular necrosis and

CC glomerulonephritis; skeletal muscle diseases including Furlenburgh's

CC disease, hypoglycaemia and obesity; gastrointestinal diseases including

CC myotonia congenita and intestinal obstruction; lymph diseases including

CC lymphoglycemia; diseases of placenta including choriocarcinoma; diseases

CC of testes including testicular cancer, male reproductive diseases

CC including low testosterone and male infertility; and disease of pancreas

CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The

CC present sequence is a polypeptide of the invention

XX Sequence 781 AA;

Query Match 100.0%; Score 92; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTVTLSDVNDNPP 18
Db 240 SGGTTVTVTLSDVNDNPP 257

RESULT 8
AAM48736
ID AAM48736 standard; protein; 781 AA.

XX AAM48736;

DT 26-MAR-2002 (first entry)

XX Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;

XX antidiabetic; neuroprotective; antiarrhythmic; antineuritic;

XX dermatological; immunosuppressive; antiinflammatory; antipruritic;

XX antidiabetic; antiallergic; antileptotic; haemostatic; antipruritic;

XX antihypertensive; antidiabetic; cardiant; antiarrhythmic;

XX anorectic; immunomodulatory; vasotropic; virucide; cyclostatic; liver;

XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;

XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;

XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;

XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;

XX gene therapy.

XX Homo sapiens.

XX WO200190145-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016013.

XX 19-MAY-2000; 2000US-0205674P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Curtis RAJ;

XX WPI: 2002-083082/11.

XX N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for

XX diagnosing and treating disorders e.g. obstructive jaundice, multiple

XX sclerosis, encephalomyelitis and atherosclerosis and to identify

XX modulators of therapeutic use.

XX Claim 9; Page 105; 119pp; English.

XX The invention relates to human cadherin family polypeptide designated

XX	OS	Homio sapiens.
XX	PN	WO000268649-A2.
XX	PD	06-SEP-2002.
XX	PF	31-JAN-2002; 2002WO-US002785.
XX	PR	31-JAN-2001; 2001US-0265395P.
XX	PR	31-JAN-2001; 2001US-0265412P.
XX	PR	31-JAN-2001; 2001US-0265517P.
XX	PR	02-FEB-2001; 2001US-0266106P.
XX	PR	05-FEB-2001; 2001US-0266767P.
XX	PR	07-FEB-2001; 2001US-0266975P.
XX	PR	07-FEB-2001; 2001US-0267057P.
XX	PR	08-FEB-2001; 2001US-0267459P.
XX	PR	09-FEB-2001; 2001US-0267823P.
XX	PR	15-FEB-2001; 2001US-0268974P.
XX	PR	26-FEB-2001; 2001US-0271664P.
XX	PR	27-FEB-2001; 2001US-0271839P.
XX	PR	27-FEB-2001; 2001US-0271855P.
XX	PR	02-MAR-2001; 2001US-0272788P.
XX	PR	02-MAR-2001; 2001US-0273046P.
XX	PR	14-MAR-2001; 2001US-0275925P.
XX	PR	14-MAR-2001; 2001US-0275947P.
XX	PR	14-MAR-2001; 2001US-0275950P.
XX	PR	14-MAR-2001; 2001US-0275989P.
XX	PR	15-MAR-2001; 2001US-0276448P.
XX	PR	15-MAR-2001; 2001US-0276450P.
XX	PR	16-MAR-2001; 2001US-0276397P.
XX	PR	16-MAR-2001; 2001US-0276768P.
XX	PR	20-MAR-2001; 2001US-0278652P.
XX	PR	26-MAR-2001; 2001US-0278775P.
XX	PR	26-MAR-2001; 2001US-0278778P.
XX	PR	29-MAR-2001; 2001US-0279882P.
XX	PR	29-MAR-2001; 2001US-0279884P.
XX	PR	30-MAR-2001; 2001US-0280147P.
XX	PR	11-APR-2001; 2001US-0282992P.
XX	PR	11-APR-2001; 2001US-0283083P.
XX	PR	20-APR-2001; 2001US-0285133P.
XX	PR	23-APR-2001; 2001US-0285749P.
XX	PR	03-MAY-2001; 2001US-0288327P.
XX	PR	03-MAY-2001; 2001US-0288564P.
XX	PR	29-MAY-2001; 2001US-0294047P.
XX	PR	30-MAY-2001; 2001US-0294473P.
XX	PR	08-JUN-2001; 2001US-0296964P.
XX	PR	18-JUN-2001; 2001US-0298959P.
XX	PR	19-JUN-2001; 2001US-0299344P.
XX	PR	13-AUG-2001; 2001US-0312020P.
XX	PR	16-AUG-2001; 2001US-0312889P.
XX	PR	16-AUG-2001; 2001US-0312908P.
XX	PR	21-AUG-2001; 2001US-0313390P.
XX	PR	28-AUG-2001; 2001US-0315470P.
XX	PR	31-AUG-2001; 2001US-0316447P.
XX	PR	07-SEP-2001; 2001US-0318115P.
XX	PR	07-SEP-2001; 2001US-0318118P.
XX	PR	12-SEP-2001; 2001US-0318740P.
XX	PR	19-SEP-2001; 2001US-0323379P.
XX	PR	18-OCT-2001; 2001US-0330245P.
XX	PR	18-OCT-2001; 2001US-0330308P.
XX	PR	14-NOV-2001; 2001US-0332701P.
XX	PA	(CURA-) CURAGEN CORP.
XX	PI	Tchernen VT, Spytek KA, Zetnusen BD, Patturajan M, Shinkets RA;
XX	PI	Li L, Gangolli EA, Padigam M, Anderson DM, Rastelli L, Miller CE;
XX	PI	Gerlach UV, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pera CEA;
XX	PI	Furtak K, Grose KW, Alebrook JP, Lepley DM, Rieger DK, Burgess CE
XX	WPI	WPI; 2002-7066998/76.
XX	DR	N-PSDB; ADI16603.

[illegible]

PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 PA (INCYTE GENOMICS INC.
 PI Burford N, Warren BA, Dugan BM, Mason PW, Richardson TW, Yue H;
 PI Forsythe JF, Elliott VS, Griffin JA, Gorvay AE, Azimzai Y;
 PI Kallack DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
 XX
 DR WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 PS
 PS Claim 1; Page 192-194; 234pp; English.
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 SQ Sequence 781 AA;

Query Match 100.0%; Score 92; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNPP 18
 DB 240 SGGTTVTTLSDVNDNPP 257

RESULT 13
 ADA01366
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteoporosis; antiinflammatory; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 XX 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.

XX (GENT) GENENTECH INC.
 PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 PS
 PS Claim 1; Fig 98; 307pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.

SQ Sequence 781 AA;

Query Match 100.0%; Score 92; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 9.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNPP 18
 DB 240 SGGTTVTTLSDVNDNPP 257

RESULT 14
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytosstatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003064474-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX (GENTH) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2003-605867/57.
DR N-PSDB; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 11; Fig 98; 308pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumor in a mammal, including tumors of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SGSTTVTVTLSDVNDNP 18
Db 240 SGSTTVTVTLSDVNDNP 257
RESULT 15
ADA43563
ID ADA43563 standard; protein; 781 AA.
XX ADA43563;
XX AC
XX 20-NOV-2003 (first entry)
XX DT
XX Human secreted/transmembrane polypeptide PRO34009.
XX DS
XX

KW Human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumor; lung tumor; colon tumor;
KW breast tumor; prostate tumor; rectal tumor; kidney tumor;
KW liver tumor; cytostatic; vaccine.
XX Homo sapiens.
XX US2003073196-A1.
XX
XX 17-APR-2003.
XX
XX 18-SEP-2002; 2002US-00246210.
XX
XX 04-APR-2001; 2001US-0282199P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2003-743814/70.
DR N-PSDB; ADA43562.
XX
XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT PRO21383 useful for stimulating the proliferation or differentiation of
PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS Claim 11; Fig 98; 307pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumor in a mammal, including tumors of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
SQ Sequence 781 AA;
Query Match 100.0%; Score 92; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SGSTTVTVTLSDVNDNP 18

Wed Dec 8 11:46:21 2004

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Page 11

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Job time : 7.44864 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 18.3932 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-12
Perfect score: 92
Sequence: 1 SGSTVTWTLSDVNDNP 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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9: /cgnt_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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12: /cgnt_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgnt_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgnt_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgnt_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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18: /cgnt_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
19: /cgnt_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
20: /cgnt_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	18	10	US-09-788-051-11
2	92	100.0	18	10	US-09-788-051-12
3	92	100.0	493	15	US-10-072-012-482
4	92	100.0	607	15	US-10-258-951-74
5	92	100.0	620	10	US-09-788-051-7
6	92	100.0	636	10	US-09-788-051-4
7	92	100.0	781	9	US-09-860-868-2
8	92	100.0	781	14	US-10-245-752-98
9	92	100.0	781	14	US-10-245-859-98
10	92	100.0	781	14	US-10-245-103-98
11	92	100.0	781	14	US-10-245-107-98
12	92	100.0	781	14	US-10-245-143-98
13	92	100.0	781	14	US-10-245-771-98

14	92	100.0	781	14	US-10-245-851-98	Sequence 98, Appl
15	92	100.0	781	14	US-10-245-883-98	Sequence 98, Appl
16	92	100.0	781	14	US-10-237-535-98	Sequence 98, Appl
17	92	100.0	781	14	US-10-238-183-98	Sequence 98, Appl
18	92	100.0	781	14	US-10-238-283-98	Sequence 98, Appl
19	92	100.0	781	14	US-10-238-370-98	Sequence 98, Appl
20	92	100.0	781	14	US-10-245-055-98	Sequence 98, Appl
21	92	100.0	781	14	US-10-245-147-98	Sequence 98, Appl
22	92	100.0	781	14	US-10-245-730-98	Sequence 98, Appl
23	92	100.0	781	14	US-10-245-739-98	Sequence 98, Appl
24	92	100.0	781	14	US-10-246-210-98	Sequence 98, Appl
25	92	100.0	781	14	US-10-239-156-98	Sequence 98, Appl
26	92	100.0	781	14	US-10-243-024-98	Sequence 98, Appl
27	92	100.0	781	14	US-10-243-409-98	Sequence 98, Appl
28	92	100.0	781	14	US-10-245-621-98	Sequence 98, Appl
29	92	100.0	781	14	US-10-245-880-98	Sequence 98, Appl
30	92	100.0	781	14	US-10-245-033-98	Sequence 98, Appl
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32	92	100.0	781	14	US-10-245-185-98	Sequence 98, Appl
33	92	100.0	781	14	US-10-245-427-98	Sequence 98, Appl
34	92	100.0	781	14	US-10-245-473-98	Sequence 98, Appl
35	92	100.0	781	14	US-10-245-770-98	Sequence 98, Appl
36	92	100.0	781	14	US-10-245-877-98	Sequence 98, Appl
37	92	100.0	781	14	US-10-246-976-98	Sequence 98, Appl
38	92	100.0	781	14	US-10-243-320-98	Sequence 98, Appl
39	92	100.0	781	14	US-10-162-435-13	Sequence 13, Appl
40	92	100.0	781	14	US-10-242-743-98	Sequence 98, Appl
41	92	100.0	781	14	US-10-242-845-98	Sequence 98, Appl
42	92	100.0	781	14	US-10-237-636-98	Sequence 98, Appl
43	92	100.0	781	14	US-10-238-325-98	Sequence 98, Appl
44	92	100.0	781	14	US-10-238-346-98	Sequence 98, Appl
45	92	100.0	781	14	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-11
; Sequence 11, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiayun
; APPLICANT: Aterburn, Matthew C
; APPLICANT: Jeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Dimauc, Renjée T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES
; FILE REFERENCE: HTS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent version 3.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-051-11
Query Match 100.0%; Score 92; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Gaps 0;
1 SGSTVTWTLSDVNDNP 18
|||||

Db 1 SGGTIVTVTLSDVNDNMP 18

RESULT 2

US-09-788-051-12
Sequence 12, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dimaec, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-12

Query Match 100.0%; Score 92; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNMP 18
Db 1 SGGTIVTVTLSDVNDNMP 18

RESULT 3
US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spyrek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patutajan, Weera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Bsha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Colman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 482
LENGTH: 493
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-482

Query Match 100.0%; Score 92; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNMP 18
Db 240 SGGTIVTVTLSDVNDNMP 257

RESULT 4
US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoqing
APPLICANT: Kohnick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50025
CURRENT APPLICATION NUMBER: US/10/258,951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 92; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNMP 18
DB 240 SGGTTVTTLSDVNDNMP 257

RESULT 5
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Dmanac, Radolje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: POLYNUCLEOTIDES
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 92; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNMP 18
DB 224 SGGTTVTTLSDVNDNMP 241

RESULT 6
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Dmanac, Radolje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: POLYNUCLEOTIDES
; FILE REFERENCE: HYS-38
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 92; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNMP 18
DB 240 SGGTTVTTLSDVNDNMP 257

RESULT 7
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 92; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTTVTTLSDVNDNMP 18
DB 240 SGGTTVTTLSDVNDNMP 257

RESULT 8
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C6
; CURRENT APPLICATION NUMBER: US/10/245,752
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24

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/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO: 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-752-98
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Query Match      100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SGGTIVTILSDVNDNP 18
Db      240 SGGTIVTILSDVNDNP 257
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RESULT 9
US-10-245-859-98
/ Sequence 98, Application US/10245859
/ Publication No. US20030064474A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Hong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245, 859
/ PRIOR FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO: 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-859-98
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Query Match      100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SGGTIVTILSDVNDNP 18
Db      240 SGGTIVTILSDVNDNP 257
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RESULT 10
US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication No. US2003006878A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Phillippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Hong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C12
/ CURRENT APPLICATION NUMBER: US/10/245, 103
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO: 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-103-98
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Query Match      100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SGGTIVTILSDVNDNP 18
Db      240 SGGTIVTILSDVNDNP 257
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/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-771-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
DB 240 SGGTIVTTLSDVNDNPP 257

RESULT 14
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/ Sequence 98, Application US/10245851
/ Publication No. US20030068782A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245, 851
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98
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/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98

Query Match          100.0%; Score 92; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTTLSDVNDNPP 18
DB 240 SGGTIVTTLSDVNDNPP 257

RESULT 15
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/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Matande, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245, 883
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98
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Wed Dec 8 11:46:22 2004

us-09-788-051-12.rapb

Page 7

QY 1 SGSTVTVTLSDVNDNP 18
Db 240 SGSTVTVTLSDVNDNP 257

Search completed: December 8, 2004, 11:34:29
Job time : 18.3932 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 2.1464 Seconds
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Title: US-09-788-051-12
Percent score: 92
Sequence: 1 SGSTVTVTLSVDVNDNP 18

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Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	83	90.2	109 3 US-09-187-859-17	Sequence 17, Appl
2	83	90.2	109 4 US-09-839-542B-17	Sequence 17, Appl
3	83	90.2	109 4 US-09-535-852-17	Sequence 17, Appl
4	83	90.2	532 1 US-08-188-228-44	Sequence 44, Appl
5	83	90.2	532 1 US-08-332-638-44	Sequence 44, Appl
6	83	90.2	793 1 US-08-188-228-54	Sequence 44, Appl
7	83	90.2	793 1 US-08-332-643-48	Sequence 54, Appl
8	83	90.2	793 1 US-08-332-638-54	Sequence 54, Appl
9	83	90.2	799 1 US-08-188-228-42	Sequence 42, Appl
10	83	90.2	799 1 US-08-332-638-42	Sequence 42, Appl
11	82	89.1	109 3 US-09-187-859-11	Sequence 11, Appl
12	82	89.1	109 4 US-09-839-542B-11	Sequence 11, Appl
13	82	89.1	109 4 US-09-535-852-11	Sequence 11, Appl
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15	80	87.0	109 3 US-09-187-859-23	Sequence 23, Appl
16	80	87.0	109 4 US-09-839-542B-8	Sequence 8, Appl
17	80	87.0	109 4 US-09-839-542B-23	Sequence 23, Appl
18	80	87.0	109 4 US-09-535-852-8	Sequence 8, Appl
19	80	87.0	109 4 US-09-535-852-23	Sequence 23, Appl
20	80	87.0	653 1 US-08-188-228-46	Sequence 46, Appl
21	80	87.0	653 1 US-08-332-638-46	Sequence 46, Appl
22	79	85.9	109 3 US-09-187-859-5	Sequence 5, Appl
23	79	85.9	109 4 US-09-839-542B-5	Sequence 5, Appl
24	79	85.9	109 4 US-09-535-852-5	Sequence 5, Appl
25	79	85.9	615 2 US-08-738-349-12	Sequence 12, Appl
26	79	85.9	693 2 US-08-738-349-6	Sequence 6, Appl
27	79	85.9	693 4 US-09-929-497-55	Sequence 55, Appl

28	79	85.9	796 1 US-08-188-228-58	Sequence 58, Appl
29	79	85.9	796 1 US-08-332-643-52	Sequence 52, Appl
30	79	85.9	796 1 US-08-332-638-58	Sequence 58, Appl
31	79	85.9	796 2 US-08-738-348-2	Sequence 2, Appl
32	79	85.9	796 2 US-08-738-348-4	Sequence 4, Appl
33	79	85.9	796 4 US-09-654-328-2	Sequence 15, Appl
34	71	77.2	109 3 US-09-187-859-15	Sequence 15, Appl
35	71	77.2	109 4 US-09-839-542B-15	Sequence 15, Appl
36	71	77.2	109 4 US-09-535-852-15	Sequence 15, Appl
37	71	77.2	794 1 US-08-188-228-60	Sequence 60, Appl
38	71	77.2	794 1 US-08-332-643-54	Sequence 54, Appl
39	71	77.2	794 1 US-08-332-638-60	Sequence 60, Appl
40	62	67.4	148 1 US-07-998-003A-36	Sequence 36, Appl
41	62	67.4	148 1 US-08-453-274B-36	Sequence 36, Appl
42	62	67.4	148 1 US-08-453-695A-36	Sequence 36, Appl
43	62	67.4	148 1 US-08-268-161A-36	Sequence 36, Appl
44	62	67.4	148 2 US-08-453-702A-36	Sequence 36, Appl
45	62	67.4	148 3 US-09-099-639-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-09-187-859-17
Sequence 17, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086, 407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-17

Query Match 90.2%; Score 83; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 16-05; 1; Indels 0; Gaps 0;
Matches 15; Conservative 2; Mismatches 1;

Qy 1 SGSTVTVTLSVDVNDNP 18
Db 90 SGSTVTVTLSVDVNDNP 107

RESULT 2
US-09-839-542B-17
Sequence 17, Application US/09839542B
Patent No. 656996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086, 407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-839-542B-17

Query Match 90.2%; Score 83; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGGTTVTTLSDVNDNPP 18
DB 90 SGGTTVTTLSDVNDNPP 107

RESULT 3
US-09-535-852-17
Sequence 17, Application US/09555852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-535-852-17

Query Match 90.2%; Score 83; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGGTTVTTLSDVNDNPP 18
DB 90 SGGTTVTTLSDVNDNPP 107

RESULT 4
US-08-188-228-44
Sequence 44, Application US/08/88228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 90.2%; Score 83; DB 1; Length 532;
Best Local Similarity 83.3%; Pred. No. 6.7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTTVTTLSDVNDNPP 18
DB 257 SGGTTVTTLSDVNDNPP 274

RESULT 5
US-08-332-638-44
Sequence 44, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 90.2%; Score 83; DB 1; Length 532;
Best Local Similarity 83.3%; Pred. No. 6.7e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTTVTTLSDVNDNPP 18

Db 257 SGTTLVTLTVDVNDNP 274

RESULT 6
US-08-188-228-54
Sequence 54, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-54

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTTLVTLTSPVNDNP 18
Db 250 SGTTLVTLTVDVNDNP 267

RESULT 7
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5638634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5638634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTTLVTLTSPVNDNP 18
Db 250 SGTTLVTLTVDVNDNP 267

RESULT 8
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01 NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 90.2%; Score 83; DB 1; Length 793;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTLSDVNDNP 18
DB 257 SGTTLVTLVDVNDNP 267

RESULT 9
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTLSDVNDNP 18
DB 257 SGTTLVTLVDVNDNP 274

RESULT 10
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borum
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 90.2%; Score 83; DB 1; Length 799;
Best Local Similarity 83.3%; Pred. No. 0.00011;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTLSDVNDNP 18
DB 257 SGTTLVTLVDVNDNP 274

RESULT 11
US-09-187-859-11
Sequence 11, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086, 407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-187-859-11

Query Match 89.1%; Score 82; DB 3; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTISVTIVTLTDVNDNPP 107

RESULT 12
US-09-839-542B-11
Sequence 11, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-839-542B-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTISVTIVTLTDVNDNPP 107

RESULT 13
US-09-535-852-11
Sequence 11, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James M.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Gallus gallus
US-09-535-852-11

Query Match 89.1%; Score 82; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18

DB 90 SGTISVTIVTLTDVNDNPP 107

RESULT 14
US-09-187-859-8
Sequence 8, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-187-859-8

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTIVTVTLTDVNDNPP 107

RESULT 15
US-09-187-859-23
Sequence 23, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 109
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-187-859-23

Query Match 87.0%; Score 80; DB 3; Length 109;
Best Local Similarity 77.8%; Pred. No. 3e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTIVTVTLSDVNDNPP 18
DB 90 SGTIVTVTLTDVNDNPP 107

Search completed: December 8, 2004, 10:01:14
Job time : 3.1464 secs

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 / Search time 3.88:194 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243

Sequence: 1 DVASVRAVAVQDAPEPPAFQ.....ENKAPGLVQISADLDP 48

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	112	46.1	793	2	D38992
2	108	44.4	796	2	A38992
3	108	44.4	796	2	I48277
4	108	44.4	796	2	I49556
5	108	44.4	796	2	A53584
6	106	43.6	794	2	I59372
7	102	42.0	785	2	I50180
8	101	41.6	790	2	I37016
9	99	40.7	789	2	I52701
10	97.5	40.1	5147	1	IJFFTM
11	95	39.1	790	2	I50178
12	95	39.1	814	2	G02878
13	92	37.9	790	2	G02678
14	91	37.4	790	2	I51638
15	90.5	37.2	701	2	T17243
16	85.5	35.2	871	2	S47518
17	84.5	34.8	896	2	I45858
18	84.5	34.8	826	2	B55363
19	84.5	34.8	896	2	A55363
20	84.5	34.8	1072	2	T00041
21	81.5	33.5	784	1	IJHUC5
22	81.5	33.5	893	1	IJHUC5
23	81.5	33.5	863	1	IJHUC5
24	80.5	33.1	1069	2	T00043
25	80.5	33.1	1544	2	T29482
26	80.5	33.1	847	1	IJHUC5
27	80.5	33.1	901	1	IJHUC5
28	79	32.5	770	2	B48910
29	79	32.5	824	2	A48910

30	79	32.5	840	2	I37281	Desla precursor -
31	79	32.5	894	2	I37282	Desla precursor -
32	79	32.5	2163	2	T15276	hypothetical prote
33	78.5	32.3	3097	2	T00021	DN-cadherin - fru
34	77.5	31.9	4351	2	T00252	MEG1 protein - fru
35	77	31.7	761	1	IJBODE	desmocollin 1a - b
36	77	31.7	839	1	IJBODE	desmocollin 1b pre
37	76	31.3	1200	2	T00042	BH-protocadherin p
38	75	30.9	827	2	A53954	Li-cadherin precurs
39	74.5	30.7	889	2	T09055	protocadherin 68 -
40	74.5	30.7	1180	2	T31066	vascular cadherin -
41	72.5	29.8	732	1	IJHUCB	B-cadherin precurs
42	72	29.6	730	1	IJHUCB	M-cadherin - mouse
43	71	29.2	877	1	IJHUCN	N-cadherin precurs
44	71	29.2	906	1	IJHUCN	cadherin 2 precurs
45	71	29.2	912	1	IJHUCN	N-cadherin precurs

ALIGNMENTS

RESULT 1
D38992
cadherin 8 - human
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C:Accession: D38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305, MUID:91283540, PMID:2059658
A:Accession: D38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-793 <SUZ>
A:Cross-references: GB:I34060; NID:G506411; PIDN:AAA35628.1; PID:G506412
C:Genetics:
A:Gene: GDB:CDH8
A:Cross-references: GDB:5822911
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:I63-269/Domain: cadherin repeat homology <CDH>

Query Match 46.1%; Score 112; DB 2; Length 793;
Best local similarity 45.7%; Pred. No. 5.1e-05;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
DB 1 DVASVRAVAVQDAPEPPAFQAAVHLTVPENKAPGLVQISADLDP 46
367 DTAIVKIVEDADEPFPVSSPTVLEVHEVAALNSVIGVTARDPD 412
RESULT 2
A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: A38992
R:Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305, MUID:91283540, PMID:2059658
A:Accession: A38992
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <SUZ>
A:Cross-references: UNIPROT:P55287; GB:I34056; NID:G506403; PIDN:AAA35622.1; PID:G506404
C:Genetics:
A:Gene: GDB:CDH11; OB
A:Cross-references: GDB:512891; OMIM:600023
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology

F:4610-5147/Domain: intracellular #status predicted <INT>

Query Match

Best Local Similarity 40.1%; Score 97.5; DB 1; Length 5147;
Matches 21; Conservative 5; Mismatches 21; Indels 1; Gaps 1;

QY 2 VASVAVADABE-PPAFQAAVHLTVENKAPGTLVGQISAADLDS 48

Db 3317 VAMLTITLVNDNPPVFNHKEVHCYIPENKPVGFVFOAHATDSDP 3364

RESULT 11

cadherin-6B - chicken

C/Species: Gallus gallus (chicken)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I50178

R:Nakagawa, S.; Takeichi, M.

Development 121, 1321-1332, 1995

A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec

A/Reference number: I50178; MID:95309115; PMID:7540531

A/Accession: I50178

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-790 <NA>

A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BAA07720.1; PID:9867998

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity 39.1%; Score 95; DB 2; Length 790;
Matches 17; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVASVAVADABEPPAFQAAVHLTVENKAPGTLVGQISAADLDS 47

Db 366 DSATRIQVEDVDEPPVFSRPATILEKEDVFINSGIVTAQDPDA 412

RESULT 12

cadherin-15 precursor - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C/Accession: G02878

R:Shimoyama, Y.

submitted to GenBank, February 1996

A/Reference number: H01775

A/Accession: G02878

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-814 <SH1>

A/Cross-references: UNIPROT:P55291; GB:D83542; NID:91208423; PIDN:BAA12012.1; PID:912084

C/Genetics:

A/Gene: CDH15; CDH14; CDH3

A/Cross-references: GDB:391031; OMIM:114019

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

F:1-17/Domain: signal sequence #status predicted <SIG>

F:155-260/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity 39.1%; Score 95; DB 2; Length 814;
Matches 21; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY 3 ASVAVADABEPPAFQAAVHLTVENKAPGTLVGQISAADLDS 47

Db 360 AKVRQVODTNEPVPFOENP.LRTSLAEGAPGTLVATRSADDPD 404

RESULT 13

G02678

cadherin-14 - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C/Accession: G02678

R:Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.

submitted to the EMBL Data Library, May 1996

A/Reference number: H01584

A/Accession: G02678

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-790 <SH1>

A/Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:91389652; PIDN:AAB02933.1; PID:913

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity 37.9%; Score 92; DB 2; Length 790;
Matches 19; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 1 DVASVAVADABEPPAFQAAVHLTVENKAPGTLVGQISAADLDS 47

Db 366 DATMKITVGDVDEPPLFSMPSTLMVYNATIGTVGTLAQDPDS 412

RESULT 14

cadherin - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: I51638

R:Espebeth, A.; Johnson, E.; Kintner, C.

Mol. Cell. Neurosci. 6, 199-212, 1995

A>Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mol

A/Accession: I51638

A/Reference number: I51638; MID:96039533; PMID:7496627

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-790 <ESP>

A/Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CAA59679.1; PID:9854

C/Superfamily: cadherin; cadherin repeat homology

F:161-267/Domain: cadherin repeat homology <CR2>

Query Match

Best Local Similarity 37.4%; Score 91; DB 2; Length 790;
Matches 19; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 DVASVAVADABEPPAFQAAVHLTVENKAPGTLVGQISAADLDS 47

Db 365 DITSVHITVEDVDEPPVFSRSFYFVENSVDIGTTIQVSAKDPA 411

RESULT 15

hypothetical protein DKFP586B021.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T17243

R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A/Reference number: T17243

A/Accession: T17243

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-701 <KOE>

A/Cross-references: UNIPROT:Q9Y5E4; EMBL:AL117449

A/Experimental source: adult uterus; clone DKFP586B0217

C/Genetics:

A/Note: DKFP586B021.1

QY 4 SVAVADABE-PPAFQAAVHLTVENKAPGTLVGQISAADLDS 47

Wed Dec 8 11:46:24 2004

us-09-788-051-13.rpr

Page 5

Db 341 NITVLVSDVNDNAPAFQTOSTYTLFVRENNSPALHIGSVSATDRDS 385

Search completed: December 8, 2004, 10:27:08
Job time : 3.88194 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.2397 Seconds
(without alignments)
1435,471 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243

Sequence: 1 DVASRVAVQDAPBPAPFTQ.....ENKAPGLVQGISADLDSF 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	100.0	370	086T00	086T00 homo sapien
2	243	100.0	493	096LQ7	096LQ7 homo sapien
3	243	100.0	819	CAD6_HUMAN	086U00 homo sapien
4	227	93.4	781	06PFX6	06PFX6 mus musculu
5	227	93.4	781	AAH57373	AAH57373 mus muscu
6	113	46.5	792	CAD6_CHICK	093119 gallus gall
7	112	46.1	508	06PAN4	06PAN4 mus musculu
8	112	46.1	508	AAH60200	AAH60200 mus muscu
9	112	46.1	519	090425	090425 brachydact
10	112	46.1	716	08C375	08C375 mus musculu
11	112	46.1	716	08C449	08C449 mus musculu
12	112	46.1	716	AAH57581	AAH57581 mus muscu
13	112	46.1	754	06BRK4	06BRK4 mus musculu
14	112	46.1	799	CAD6_HUMAN	055286 homo sapien
15	112	46.1	799	CAD6_MOUSE	P97291 mus musculu
16	112	46.1	799	CAD6_RAT	054600 rattus norv
17	111	45.7	796	096C29	096C29 homo sapien
18	109	44.9	789	CAD9_HUMAN	Q9UB44 homo sapien
19	108	44.4	796	CAD6_HUMAN	P55287 homo sapien
20	108	44.4	796	CAD6_MOUSE	P55288 mus musculu
21	108	44.4	796	08C706	08C706 mus musculu
22	106	43.6	794	CAD6_HUMAN	P55289 homo sapien
23	106	43.6	794	086UD2	086UD2 homo sapien
24	102	42.0	551	08AWW2	08AWW2 gallus gall
25	102	42.0	785	CAD7_CHICK	Q90763 gallus gall
26	102	42.0	794	093264	Q93264 xenopus lae
27	101.5	41.8	5147	FAT_DROME	P31450 drosophila
28	101	41.6	790	CAD6_HUMAN	P55280 rattus norv
29	99	40.7	789	CAD6_RAT	094260 xenopus lae
30	99	40.7	792	09DF80	09DF80 xenopus lae
31	99	40.7	792	09DF81	09DF81 xenopus lae

32	97.5	40.1	794	2	Q925L0	Q925L0 mus musculu
33	97.5	40.1	931	1	CDG3_HUMAN	Q9Y5H4 homo sapien
34	97	39.9	786	1	CAD6_HUMAN	Q9Y6H8 homo sapien
35	97	39.9	788	2	08CWS7	08CWS7 mus musculu
36	97	39.9	788	2	08VI68	08VI68 mus musculu
37	97	39.9	788	2	AAH62962	AAH62962 mus muscu
38	97	39.9	789	1	CAD6_CHICK	P79955 gallus gall
39	97	39.9	801	1	CAD6_HUMAN	Q9HBT6 homo sapien
40	95	39.1	790	1	CAD6_CHICK	Q90762 gallus gall
41	95	39.1	814	1	CAD6_HUMAN	P55291 homo sapien
42	94.5	38.9	794	2	08C8Z3	08C8Z3 mus musculu
43	94.5	38.9	794	2	09IXZ8	09IXZ8 mus musculu
44	93.5	38.5	787	1	CDBF_HUMAN	Q9Y5E8 homo sapien
45	93.5	38.5	829	2	08BN17	08BN17 mus musculu

ALIGNMENTS

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RESULT 1
ID 086T00 PRELIMINARY; PRT; 370 AA.
AC 086T00;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Full-length cDNA clone CSODK003Y017 of Hela cells of Homo sapiens
DE (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hela cells;
RA Li W.B., Gruber C., Jesses J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hela cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 4 cadherin domains.
EMBL BX248303; CAD62630.1; -
GO GO:0016020; C:membrane; IEA.
GO GO:0005059; F:calcium ion binding; IEA.
GO GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR Pfam: PF00028; Cadherin; 3.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 2.
DR PROSITE: PS00232; CADHERIN_1; 1.
DR PROSITE: PS0268; CADHERIN_2; 4.
KW Calcium; Calcium-binding.
FT NON TER 1
FT NON TER 370
SQ SEQUENCE 370 AA; 39479 MW; 3996D4AF8A450E80 CRC64;

Query Match 100.0%; Score 243; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPBPAPFTQAAYLTVPENKAPGLVQGISADLDSF 48
DB 118 DVASRVAVQDAPBPAPFTQAAYLTVPENKAPGLVQGISADLDSF 165

RESULT 2
ID 096LQ7 PRELIMINARY; PRT; 493 AA.
AC 096LQ7;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

```

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Hypothetical protein FLJ25193.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid.
 RA Nishikawa K., Magatsuna M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isegai T., Sugano S.
 RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK057922; BAB71613.1; -
 DR HSSP; P12830; 106S.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005039; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR SMART; SM00112; CA; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 4.
 KW Calcium; Calcium-binding.
 SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;
 Query Match 100.0%; Score 243; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVASRVAVQDAPEPPAQAAYHLTVBENKAPGLVVGQISADIDSP 48
 Db 357 DVASRVAVQDAPEPPAQAAYHLTVBENKAPGLVVGQISADIDSP 404
 RESULT 3
 CADO_HUMAN STANDARD; PRT; 819 AA.
 ID Q86UP0; Q86UP1; Q9NT84;
 AC Q86UP0; Q86UP1; Q9NT84; Created
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-24 precursor (UN02834/PRO34009).
 GN Name=CDH24; Synonyms=CDH11L;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
 RP CATENINS.
 RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
 RA Katsiarsz B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
 RT "Characterization of cadherin-24, a novel alternatively spliced type
 RT II cadherin."
 RL J. Biol. Chem. 278:27513-27519(2003).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Adaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Helens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Yagusa A.,
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yasuda D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment."
 RL Genome Res. 13:2265-2270(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Testis;
 RA Blum H., Baerensachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RU Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. Cadherin-24 mediate strong
 CC cell-cell adhesion.
 CC -1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=long form;
 CC IsoId=Q86UP0.1; Sequence=displayed;
 CC Name=2; Synonyms=short form;
 CC IsoId=Q86UP0.2; Sequence=VSP_008717;
 CC Name=3;
 CC IsoId=Q86UP0.3; Sequence=VSP_008718, VSP_008719;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC -----
 DR EMBL; AY260900; AAP20590.1; -
 DR EMBL; AY260901; AAP20591.1; -
 DR EMBL; AY358199; AA085566.1; -
 DR EMBL; AL337477; CAB70758.1; -
 DR PIR; T46418; T46418.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:14265; CDH24.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002333; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Multigene family; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19
 FT PROPEP 21 44
 FT CHAIN 45 819
 FT DOMAIN 45 641
 FT TRANSMEM 642 662
 FT DOMAIN 663 819
 FT DOMAIN 46 150
 FT DOMAIN 151 259
 FT DOMAIN 260 374
 FT DOMAIN 375 517
 FT DOMAIN 517 630
 FT CARBOHYD 446 446
 FT CARBOHYD 548 548
 FT CARBOHYD 563 563
 FT VARSPPLIC 455 492
 FT VARSLIC 1 427
 FT VARSPPLIC 428 492
 FT FTID=VSP_008718.
 FT EFTHTAAPIDREAAWNLTVLATELGMSNGPERGWPLL
 FT VAEMSAAPAPQSRVSGAVAPQ -> MNTVCTWYCSIH
 FT ALFSTCTLHAIVMCLMELVYASGIIHAAHBMHVRNVVC

FT VNRVCGVLPs (in isoform 3).
 FT /FT18-NSP 008719.
 SQ SEQUENCE 819 AA; 87751 MW; 9083034F18B7E4A CRC64;
 Query Match 100.0%; Score 243; DB 1; Length 819;
 Best Local Similarity 100.0%; Pred. No. 2.7e-20;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGOISADLSP 48
 DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGOISADLSP 404

RESULT 4
 ID Q6PX6 PRELIMINARY; PRT; 781 AA.
 AC Q6PX6;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC057373; AAH57373.1; -
 DR InterPro; IPR000216; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF000028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SO SEQUENCE 781 AA; 84104 MW; 15996D6B6C9835AA CRC64;

Query Match 93.4%; Score 227; DB 2; Length 781;
 Best Local Similarity 91.7%; Pred. No. 2.1e-18;

Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGOISADLSP 48
 DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGOISADLSP 404

RESULT 5
 ID AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373;
 DT 02-MAR-2004 (TREMBLrel. 27, Created)
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057373; AAH57373.1; -
 SO SEQUENCE 781 AA; 84104 MW; 15996D6B6C9835AA CRC64;

Query Match 93.4%; Score 227; DB 2; Length 781;
 Best Local Similarity 91.7%; Pred. No. 2.1e-18;
 Matches 44; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGOISADLSP 48
 DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGOISADLSP 404

RESULT 6
 ID Q93319 STANDARD; PRT; 792 AA.
 AC Q93319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor.
 GN Name=CDH11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feingold J., Helton E., Ketterman M., Madan A., Rodriguez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC [2]
 EN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Brain;
 RC Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 KW Calcium-binding; Calcium-binding.
 SQ SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;
 Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASRVAVVADAPAPPAQTAAHYHTVPEKAPGTLVQGISAADLD 46
 Db 374 DTAIVXIVEDADEPVPFSSPTLLVHEHNAIIVGIVTARDD 419
 RESULT 8
 ID AAH60200 PRELIMINARY; PRT; 508 AA.
 AC AAH60200;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feingold J., Helton E., Ketterman M., Madan A., Rodriguez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC [2]
 EN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Brain;
 RC Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 KW Calcium-binding; Calcium-binding.
 SQ SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;
 Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASRVAVVADAPAPPAQTAAHYHTVPEKAPGTLVQGISAADLD 46
 Db 374 DTAIVXIVEDADEPVPFSSPTLLVHEHNAIIVGIVTARDD 419
 RESULT 7
 ID O6PAN4 PRELIMINARY; PRT; 508 AA.
 AC O6PAN4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feingold J., Helton E., Ketterman M., Madan A., Rodriguez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC [2]
 EN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Brain;
 RC Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 KW Calcium-binding; Calcium-binding.
 SQ SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;
 Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASRVAVVADAPAPPAQTAAHYHTVPEKAPGTLVQGISAADLD 46
 Db 374 DTAIVXIVEDADEPVPFSSPTLLVHEHNAIIVGIVTARDD 419
 RESULT 8
 ID AAH60200 PRELIMINARY; PRT; 508 AA.
 AC AAH60200;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feingold J., Helton E., Ketterman M., Madan A., Rodriguez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC [2]
 EN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Brain;
 RC Strausberg R.,
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; BC060200; AAH60200.1; -
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS00268; CADHERIN_2; 4.
 KW Calcium-binding; Calcium-binding.
 SQ SEQUENCE 508 AA; 56388 MW; 9053F774BCF52255 CRC64;
 Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASRVAVVADAPAPPAQTAAHYHTVPEKAPGTLVQGISAADLD 46
 Db 374 DTAIVXIVEDADEPVPFSSPTLLVHEHNAIIVGIVTARDD 419
 RESULT 7
 ID O6PAN4 PRELIMINARY; PRT; 508 AA.
 AC O6PAN4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Cdh8 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliady S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfard G.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Skrimwood J., Schmutz U., Myers R.W., Butterfield Y.S.,
 RA Krzywincki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC060200; AAH60200.1; -
 SQ SEQUENCE 508 AA, 56388 MW, 9053F774BCF52255 CRC64;

Query Match 46.1%; Score 112; DB 2; Length 508;
 Best Local Similarity 45.7%; Pred. No. 7.5e-05;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPEPPAFTQAAYHLTPENKAPGTLVGQISADLD 46
 Db 374 DTTIVKIVSDADEPFPFMAFSYNFVEVENAPAGTLVGRVHADTD 119

RESULT 9
 ID 090425 PRELIMINARY; PRT; 519 AA.
 AC 090425;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Ventral neural cadherin (Fragment).
 GN Namescdh1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96363857; PubMed=8725279;
 RA Franklin U.I., Sargent T.D.;
 RT "Ventral neural cadherin, a novel cadherin expressed in a subset of
 RT neural tissues in the zebrafish embryo.";
 RL Dev. Dyn. 206:121-130(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Franklin J.L.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 3 cadherin domains.
 CC EMBL: U01419; AAB47406.1; -
 DR HSSP; P09803; 117W
 DR ZFIN; ZDB-GENE-980526-170; cdh1.1.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_3.
 DR Pfam; PF01049; Cadherin_C1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 3.
 DR PROSITE; PS00232; CADHERIN_1; 1.
 DR PROSITE; PS50268; CADHERIN_2; 3.

KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 FT NON_TER
 SQ SEQUENCE 519 AA; 57807 MW; 0D2547C3D346B28 CRC64;

Query Match 46.1%; Score 112; DB 2; Length 519;
 Best Local Similarity 45.7%; Pred. No. 7.7e-05;
 Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPEPPAFTQAAYHLTPENKAPGTLVGQISADLD 46
 Db 93 DTTIVKIVSDADEPFPFMAFSYNFVEVENAPAGTLVGRVHADTD 138

RESULT 10
 ID 08C375 PRELIMINARY; PRT; 716 AA.
 AC 08C375;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone:D930046N17 product:cadherin 8, full insert
 DE sequence.
 DE Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=92279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium,
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishize T., Hazada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-formet
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).

RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai U., Kojima Y., Kondo S., Kondo M., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagami A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK086711; BAC39724.1; -.
 DR HSSP: P15116; INCU.
 DR MGD: MG1:107434; Cdh8.
 DR GO: GO:0016020; C-membrane; IEA.
 DR GO: GO:0005509; P-calcium ion binding; IEA.
 DR GO: GO:0007156; P-photophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR Pfam: PF00028; Cadherin.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PRO0205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00332; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79149 MW; 58BD598F638624A CRC64;

 Query Match 46.1%; Score 112; DB 2; Length 716;
 Best Local Similarity 45.7%; Pred. No. 0.00011;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

 QY 1 DVASRVAVQDAPEPPATQAAYHITVENKAPGTLVQISADLD 46
 DB 374 DPAATKIVEDADEPPVSPFYLLEVENALNSVIGQVARDPD 419

 RESULT 11
 Q06449 PRELIMINARY; PRT; 716 AA.
 AC Q06449;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone: C63002D14 product: cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai U., Kojima Y., Kondo S., Kondo M., Koyama S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagami A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueberschub T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalski U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.U., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.


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RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
    (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR EMBL: AK083092; BAC38758.1; -.
DR EMBL: BC057581; AAH57581.1; -.
DR HSSP: P5116; INCU.
DR MGD: MGI:107434; Cdhr.
DR GO: GO:0016020; Cmembrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C_term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PRO0205; CADHERIN_1.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 5.
DR Calcium: Calcium-binding; Cell adhesion; Transmembrane.
KM SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 46.1%; Score 112; DB 2; Length 716;
Best Local Similarity 45.7%; Pred. No. 0.00011;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASVAVQDAPPEPAFTQAAYHLTPENKAGCTIVGOISADLD 46
DB 374 DTAIVKIVEDADPEPFSSPTLLEVENALNSVIGQYARDPD 419

RESULT 12
AAH57581 PRELIMINARY; PRT; 716 AA.
ID AAH57581;
AC AAH57581;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Cdhr protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buerger K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loggellano N.A., Peters G.J., Abremson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman W., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravinsky M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
    and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBD databases.

DR EMBL: BC057581; AAH57581.1; -.
SQ SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;

Query Match 46.1%; Score 112; DB 2; Length 716;
Best Local Similarity 45.7%; Pred. No. 0.00011;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASVAVQDAPPEPAFTQAAYHLTPENKAGCTIVGOISADLD 46
DB 374 DTAIVKIVEDADPEPFSSPTLLEVENALNSVIGQYARDPD 419

RESULT 13
Q8BRK4 PRELIMINARY; PRT; 754 AA.
ID Q8BRK4;
AC Q8BRK4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
    library, clone:A830083P13 product:cadherin 8, full insert
    sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RC MEDLINE=99279253; PubMed=10349636;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RC MEDLINE=21085660; PubMed=11217851;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium;
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
    Analysis of the mouse transcriptome based on functional annotation of
    60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RC MEDLINE=20499374; PubMed=11042159;
RX Shibata K., Itoh M., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
    Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
    Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
    prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RC MEDLINE=20530913; PubMed=11076861;
RX Shbata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
    Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
    Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
    Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
    Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Obara E., Watanaka M.,
    Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
    Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-394-format
    sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
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RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashita K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanakawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Mizuta M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shitaki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK044046; BAC31751.1; -.
 DR HSSP: P5116; INCT.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005029; P:calcium ion binding; IEA.
 DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Calcutm: Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;
 SQ
 Query Match 46.1%; Score 112; DB 1; Length 754;
 Best Local Similarity 45.7%; Pred. No. 0.00012;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASVAVAVQDAPEPAFTQAAVHLTVENKAPGTLVQGISADLD 46
 DB 374 DVAIVAVEDADEPVPFSSPTLVLEVENNALNSVIGVATRPDD 419
 RESULT 14
 CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P55286; O9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitaajima M., Natori M.,
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins";
 RL Biochem. J. 349:159-167(2000).
 RN [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=95073006; PubMed=7982033;
 RA Tanhara H., Sano K., Heilmark R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [3]

RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanhara H.,
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue";
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Mainly expressed in brain. Found in certain
 CC nerve cell lines, such as retinoblasts, glioma cells and
 CC neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL: AB035305; BA87419.1; -.
 DR EMBL: L34060; AA35628.1; ALT_INIT.
 DR HSSP: P09803; 117W.
 DR Genew: HGNC:1767; CDH8.
 DR MIM: 603008; -.
 DR GO: GO:0007155; P:cell adhesion; TAS.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR Calcutm: Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 62 167 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 355 355 V -> D (in Ref. 2 and 3).
 FT CONFLICT 647 647 H -> HQ (in Ref. 2 and 3).
 SQ SEQUENCE 799 AA; 88253 MW; 9B119B86039CA0A CRC64;
 Query Match 46.1%; Score 112; DB 1; Length 799;
 Best Local Similarity 45.7%; Pred. No. 0.00012;
 Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVASVAVAVQDAPEPAFTQAAVHLTVENKAPGTLVQGISADLD 46
 DB 374 DVAIVAVEDADEPVPFSSPTLVLEVENNALNSVIGVATRPDD 419
 RESULT 15
 CAD8 MOUSE

Search completed: December 8, 2004, 10:24:40
Job time : 20.2397 secs

ID CAD8 MOUSE STANDARD; PRT; 799 AA.
AC P97251;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-8 precursor.
GN Name=Cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=97174321; PubMed=9022055;
RA Korematu K., Redies C.;
RT "Restricted expression of cadherin-8 in segmental and functional
subdivisions of the embryonic mouse brain.";
RL Dev. Dyn. 208:178-189(1997).
CC -!- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X85600; CAA64857.1; -.
DR HSSP: P09803; 117W.
DR MGD; MG1:107434; Cdh8.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; Cadherin; 5.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
KW Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 61 Potential.
FT CHAIN 62 799 Cadherin-8.
FT DOMAIN 62 621 Extracellular (Potential).
FT TRANSMEM 622 642 Potential.
FT TRANSWEM 643 799 Cytoplasmic (Potential).
FT DOMAIN 642 799 Potential.
FT DOMAIN 62 167 Cadherin 1.
FT DOMAIN 168 276 Cadherin 2.
FT DOMAIN 277 391 Cadherin 3.
FT DOMAIN 392 494 Cadherin 4.
FT DOMAIN 495 616 Cadherin 5.
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 473 473 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 544 544 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;

Query Match 46.1%; Score 112; DB 1; Length 799;
Best Local Similarity 45.7%; Pred. No. 0.00012;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

OY 1 DVASVAVADAPAPPAQTQAAVHLTPENKAPGTIVGQISAADL 46
DB 374 DTAIVKIVEDADEPVPSSPTLLEVENAALNSVIGVTARDPD 419

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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 19.863 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-13
Sequence: 1 DVASRYVAVQDAPEPPAFTQ.....ENKAFGLVQISADDDSP 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358723299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.23sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	243	100.0	48	ADD29454 Human cad
2	243	100.0	193	ADD29456 Human cad
3	243	100.0	493	AD116946 Human NOV
4	243	100.0	607	ABBS3295 Human NOV
5	243	100.0	620	ADD29448 Human cad
6	243	100.0	636	ADD29445 Human cad
7	243	100.0	781	ABBS3296 Human pol
8	243	100.0	781	AAW48736 Human cad
9	243	100.0	781	ABG34078 Human PRO
10	243	100.0	781	AD116604 Human NOV
11	243	100.0	781	AD116606 Human NOV
12	243	100.0	781	ABR40114 Human cel
13	243	100.0	781	ADA01356 Human PRO
14	243	100.0	781	ADA43795 Human sec
15	243	100.0	781	ADA43563 Human sec
16	243	100.0	781	ADA01238 Human PRO
17	243	100.0	781	ADA01122 Human sec
18	243	100.0	781	ADA43679 Human sec
19	243	100.0	781	ADA06941 Human PRO
20	243	100.0	781	ADA08439 Novel hum
21	243	100.0	781	ADB89722 Human PRO
22	243	100.0	781	ADB87005 Human PRO
23	243	100.0	781	ADB66160 Human sec
24	243	100.0	781	ADB89838 Human PRO
25	243	100.0	781	ADB89493 Novel hum

26	243	100.0	781	ADB66044 Human sec
27	243	100.0	781	ADC23442 Human tra
28	243	100.0	781	ADC26135 Human PRO
29	243	100.0	781	ADB04962 Human PRO
30	243	100.0	781	ADB11268 Human PRO
31	243	100.0	781	ADB88199 Human PRO
32	243	100.0	781	ADDS5494 Human sec
33	243	100.0	781	ADB06424 Human PRO
34	243	100.0	781	ADB38199 Human PRO
35	243	100.0	781	ADB88315 Human PRO
36	243	100.0	781	ADD90896 Human sec
37	243	100.0	781	ADF99451 Human sec
38	243	100.0	781	ADG06544 Human PRO
39	243	100.0	781	ADG05495 Human PRO
40	243	100.0	781	ADG82496 Human PRO
41	243	100.0	781	ADE51749 Human sec
42	243	100.0	781	ADE51865 Human sec
43	243	100.0	781	ADE37723 Human sec
44	243	100.0	781	ADE37607 Human sec
45	243	100.0	781	ADD95378 Human sec

ALIGNMENTS

RESULT 1	ADD29454	ADD29454 standard; protein; 48 AA.
ID	ADD29454	
XX	ADD29454;	
AC	ADD29454;	
XX		
DT	15-JAN-2004	(first entry)
XX		
DE	Human cadherin-like protein peptide fragment Seq ID13.	
XX		
KX	cadherin-like protein; transmembrane protein; cadherin domain;	
KW	homotypic cell-cell adhesion; cytoskeletal; osteopetrotic; cancer;	
KM	osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrotosis;	
KX	metastatic tumour; human.	
XX		
OS	Homo sapiens.	
XX		
PN	US2003144491-A1.	
XX		
PD	31-JUN-2003.	
XX		
PF	16-FEB-2001; 2001US-00788051.	
XX		
PR	03-FEB-2000; 2000US-00496914.	
PR	27-APR-2000; 2000US-00560875.	
XX		
PA	(GDB//) GODBOLE S D.	
PA	(KXOC//) KUO C.	
PA	(ART//) ARTERBURN M C.	
PA	(YRUN//) YOUNG G.	
PA	(PALE//) PALENCIA S.	
PA	(TANG//) TANG Y T.	
PA	(LIUC//) LIU C.	
PA	(DRMA//) DRMANAC R T.	
XX		
PI	Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YF,	
PI	Liu C, Drmanac RT;	
XX		
DR	WPI, 2003-829799/77.	
XX		
PT	Novel isolated human secreted cadherin-like polypeptide useful for	
PT	treating diseases such as cancers, osteoporosis, Paget's disease,	
PT	osteomalacia, hyperostosis, osteopetrotosis.	
XX		
PS	Claim 11, SEQ ID NO 13; 63pp; English.	
XX		
CC	This invention relates to a novel isolated human secreted cadherin-like	
CC	protein and the DNA sequence which encodes it. Cadherins are a family of	

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

XX
SQ Sequence 48 AA;

Query Match 100.0%; Score 243; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.3e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQGISADIDSP 48
DB 1 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQGISADIDSP 48

RESULT 2

ID ADD29456 standard; protein, 193 AA.

XX
AC ADD29456;

DT 15-JAN-2004 (first entry)

XX Human cadherin-like protein peptide fragment Seq ID15.

XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
metastatic tumour; human.

XX Homo sapiens.

XX US200314491-A1.

XX 31-JUL-2003.

XX 16-FEB-2001; 2001US-00788051.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (GODB/) GODBOLE S D.

XX (KUOC/) KUO C.

XX (ARTE/) ARTERBURN M C.

XX (YEUN/) YEUNG G.

XX (PALE/) PALENCIA S.

XX (TANG/) TANG Y T.

XX (LIUC/) LIU C.

XX (DRMA/) DRMANAC R T.

XX Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,

XX Liu C, Drmanac RT;

XX WPI; 2003-829793/77.

XX N-PSDB; ADD29460.

XX Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11, SEQ ID NO 15; 63bp; English.

XX This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their

extracellular region. The extracellular portion mediates homotypic cell-cell adhesion that is calcium dependent. Modulators of the protein of the invention may have cytosolic or osteopathic activity. The invention may allow development of therapeutics useful for the treatment of diseases such as cancers, osteoporosis, Paget's disease, osteomalacia, hyperostosis and osteopetrosis. The protein and DNA sequence of the invention may also be useful as markers for prognosis of metastatic tumours. The present sequence is that of a peptide fragment of the human secreted cadherin-like protein which was used during the exemplification of the invention.

XX
SQ Sequence 193 AA;

Query Match 100.0%; Score 243; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQGISADIDSP 48
DB 96 DVASVRVAVQDAPEPPAFTQAAVHLLTPENKAPGTLVQGISADIDSP 143

RESULT 3

ID AD116946 standard; protein, 493 AA.

XX
AC AD116946;

DT 15-APR-2004 (first entry)

XX Human NOVX protein homologue SeqID 482.

XX
KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
inflammation; autoimmune disorder; allergy; blood disorder;
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
KW Alzheimer's disease; infection; str.

XX Homo sapiens.

XX WO200268649-A2.

XX 06-SEP-2002.

XX 31-JAN-2002; 2002WO-US002785.

XX 31-JAN-2001; 2001US-0265395F.

XX 31-JAN-2001; 2001US-0265412P.

XX 31-JAN-2001; 2001US-0265514P.

XX 31-JAN-2001; 2001US-0265517P.

XX 02-FEB-2001; 2001US-0266406P.

XX 05-FEB-2001; 2001US-0266767P.

XX 07-FEB-2001; 2001US-0266775P.

XX 08-FEB-2001; 2001US-0267057P.

XX 09-FEB-2001; 2001US-0267459P.

XX 15-FEB-2001; 2001US-0267823P.

XX 26-FEB-2001; 2001US-0268974P.

XX 27-FEB-2001; 2001US-0271839P.

XX 27-FEB-2001; 2001US-0271835P.

XX 02-MAR-2001; 2001US-0272788P.

XX 12-MAR-2001; 2001US-0273046P.

XX 14-MAR-2001; 2001US-0275925P.

XX 14-MAR-2001; 2001US-0275947P.

XX 14-MAR-2001; 2001US-0275950P.

XX 15-MAR-2001; 2001US-0275989P.

XX 15-MAR-2001; 2001US-0276448P.

XX 16-MAR-2001; 2001US-0276397P.

XX 16-MAR-2001; 2001US-0276768P.

XX 20-MAR-2001; 2001US-0278652P.

XX 26-MAR-2001; 2001US-0278775P.

XX 26-MAR-2001; 2001US-0278778P.

PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282992P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312820P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 31-AUG-2001; 2001US-0315470P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 (CUBA-) CUBAGEN CORP.
 PI Tchernev VT, Spytek KA, Zerhusen BD, Paturajan M, Shinkets RA;
 PI Li L, Gangoli EA, Padgug M, Anderson DW, Rastelli L, Miller CE;
 PI Gerlach VL, Traupler RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
 PI Furek K, Grose WM, Alschbrook JP, Lepley DM, Rieger DK, Burgess CE;
 DR WPI; 2002-706998/76.
 XX New NOXV polypeptides and nucleic acids, useful for preventing or
 PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy, or
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX Disclosure, SEQ ID NO 482; 1498bp; English.
 XX This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOXV proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOXV polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytostatic, candidant, antiinflammatory, immunosuppressive, anti-allergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antistimatic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, viricide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
 CC of the invention.
 XX Sequence 493 AA;
 SQ

Query Match 100.0%; Score 243; DB 5; Length 493;
 Best Local Similarity 100.0%; Pred. No. 6,7e-24;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DVASRVAVODAPEPPAFQTQAAVHLTPENKAGTGVGQISADLDSF 48
 DB 357 DVASRVAVODAPEPPAFQTQAAVHLTPENKAGTGVGQISADLDSF 404
 RESULT 4
 ABB53295
 ID ABB53295 standard; protein; 607 AA.
 XX
 AC ABB53295;
 DT 12-FEB-2002 (first entry)
 XX
 DE Human polypeptide #35.
 XX
 KW Human; nootropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquiliser; antiarrhythmic; cardiant; antidiabetic;
 KW antiinflammatory; antilipemic; hepatotropic; viricide; antidiabetic;
 KW nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.
 XX
 OS Homo sapiens.
 XX
 FN WC200181363-A1.
 XX
 PD 01-NOV-2001.
 XX
 PF 26-APR-2001; 2001WO-US013360.
 XX
 PR 27-APR-2000; 2000US-0199963P.
 PR 11-MAY-2000; 2000US-0203356P.
 PR 25-MAY-2000; 2000US-0207087P.
 PR 26-MAY-2000; 2000US-0207546P.
 XX
 XX (SMIR) SMITHKLINE BEECHAM CORP.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 XX
 XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 PI Lai Y, Xie Q;
 XX WPI; 2002-041392/05.
 DR N-PSDB; ABA90360.
 XX
 PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX
 PS Claim 1; Page 106-108; 116bp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 581, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Bulbular's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including

CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention
XX
SQ Sequence 607 AA;
Query Match 100.0%; Score 243; DB 5; Length 607;
Best Local Similarity 100.0%; Pred. No. 8.5e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVASVAVAVQADAPPEPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 48
DB 357 DVASVAVAVQADAPPEPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 404
RESULT 5
ADD29448
ID ADD29448 standard; protein; 620 AA.
XX
AC ADD29448;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like mature protein.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PA (GDB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
PI Liu C, Drmanac RT;
XX
DR WPI; 2003-829799/77.
XX
PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX
PS Claim 11; SEQ ID NO 7; 63pp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic

CC tumours. The present sequence is that of the mature human secreted
CC cadherin-like protein which was used during the exemplification of the
CC invention.
XX
SQ Sequence 620 AA;
Query Match 100.0%; Score 243; DB 7; Length 620;
Best Local Similarity 100.0%; Pred. No. 8.7e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVASVAVAVQADAPPEPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 48
DB 341 DVASVAVAVQADAPPEPAFTQAAYHLLTPENKAPGTLVGQISADIDSP 388
RESULT 6
ADD29445
ID ADD29445 standard; protein; 636 AA.
XX
AC ADD29445;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human cadherin-like protein amino acid sequence.
XX
KW cadherin-like protein; transmembrane protein; cadherin domain;
KW homotypic cell-cell adhesion; cytosolic; osteopathic; cancer;
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
KW metastatic tumour; human.
XX
OS Homo sapiens.
XX
PN US2003144491-A1.
XX
PD 31-JUL-2003.
XX
PF 16-FEB-2001; 2001US-00788051.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PA (GDB/) GODBOLE S D.
PA (KUOC/) KUO C.
PA (ARTE/) ARTERBURN M C.
PA (YEUN/) YEUNG G.
PA (PALE/) PALENCIA S.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (DRMA/) DRMANAC R T.
XX
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
PI Liu C, Drmanac RT;
XX
DR WPI; 2003-829799/77.
XX
PT Novel isolated human secreted cadherin-like polypeptide useful for
PT treating diseases such as cancers, osteoporosis, Paget's disease,
PT osteomalacia, hyperostosis, osteopetrosis.
XX
PS Claim 11; SEQ ID NO 4; 63pp; English.
XX
CC This invention relates to a novel isolated human secreted cadherin-like
CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutics useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of the human secreted cadherin-like
CC protein of the invention.

SO Sequence 636 AA;

Query Match 100.0%; Score 243; DB 7; Length 636;
Best Local Similarity 100.0%; Pred. No. 9e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSF 48
DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSF 404

RESULT 7
ABBS3296
ID ABBS3296 standard; protein; 781 AA.

AC ABBS3296;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #36.

XX Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquiliser; antiarrhythmic; cardiac; antiautismic;
XX antiinflammatory; antihypertensive; hepatotropic; virostatic; antidiabetic;
XX nephrotropic; anorectic; cyostatic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.

OS Homo sapiens.

PN WO200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

PR 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-020336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

PA (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

DR N-PSDB; ABA90361.

DR N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
XX and treating diseases associated with the polypeptide, e.g. Alzheimer's
XX disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PS Claim 1; Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
XX 844, 782, 282, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 285,
XX 744, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases such as neurological and psychiatric diseases including
XX Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic

CC dystrophy, anorexia and depression; cardiovascular diseases including
CC congestive heart failure, Hodgkin's disease and myocardial infarction;
CC respiratory diseases including asthma, chronic obstructive pulmonary
CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
CC renal disease including renal failure, acute tubular necrosis and
CC glomerulonephritis; skeletal muscle diseases including Eulenburg's
CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
CC myotonia congenita and intestinal obstruction; lymphomas including
CC lymphosarcoma; diseases of placenta including chorioncarcinoma; diseases
CC of testes including testicular cancer, male reproductive diseases
CC including low testosterone and male infertility; and disease of pancreas
CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
CC present sequence is a polypeptide of the invention.

SO Sequence 781 AA;

Query Match 100.0%; Score 243; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSF 48
DB 357 DVASVRVAVQDAPEPPAFQTQAAVHLTPENKAPGTLVGQISADLDSF 404

RESULT 8
AAM48736
ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

XX Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
XX antidiabetic; neuroprotective; antiarrhythmic; antipneumatic;
XX dermatological; immunosuppressive; antiinflammatory; antiporiatic;
XX antiautismic; antiallergic; antileptotic; haemostatic; antiparalytic;
XX antithyroid; hypotensive; antiarteriosclerotic; cardiac; antiarrhythmic;
XX anorectic; immunomodulatory; vasotropic; virostatic; cyostatic; liver;
XX thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
XX viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
XX osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
XX thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
XX gene therapy.

OS Homo sapiens.

PN WO200190145-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

PR 19-MAY-2000; 2000US-0205674P.

PA (MILL-) MILLENNIUM PHARM INC.

PA (MILL-) MILLENNIUM PHARM INC.

DR N-PSDB; ABA96406; ABA96407.

DR N-PSDB; ABA96406; ABA96407.

XX New human cadherin family protein and polynucleotides, useful for
XX diagnosing and treating disorders e.g. obstructive jaundice, multiple
XX sclerosis, encephalomyelitis and atherosclerosis and to identify
XX modulators of therapeutic use.

PS Claim 9; Page 105; 119pp; English.

KW chromosome mapping; tissue typing; pharmacogenomic; SNP;

RESULT	ID	AD116604	AD116604 standard; protein; 781 AA.
XX	AC	AD116604;	
XX	DT	15-APR-2004 (first entry)	
DE	XX	Human NOVX protein to treat human pathological conditions Segid140.	
KW	XX	human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;	
KW	XX	inflammation; autoimmune disorder; allergy; blood disorder;	
KW	XX	acquired immunodeficiency syndrome; AIDS; obesity; asthma;	
KW	XX	immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;	
KW	XX	Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;	
KW	XX	cytostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;	
KW	XX	hemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;	
KW	XX	antisthmatic; nephrotropic; antiarrhythmic; hepatotropic;	
KW	XX	neuroprotective; nociceptive; antibacterial; virucide; antiparasitic;	
KW	XX	relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;	
KW	XX	chromosome mapping; tissue typing; pharmacogenomic; SNP;	

XX single nucleotide polymorphism.
KM Homo sapiens.
XX WO200268649-A2.
XX 06-SEP-2002.
XX
PF 31-JAN-2002; 2002MO-US002785.
XX
XX 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265414P.
PR 31-JAN-2001; 2001US-0265417P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0276852P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278788P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282892P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312899P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313907P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330389P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernyev VT, Spytek KA, Zernhosen BD, Faturajan M, Shinkels RA,
PI Li L, Ganggoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE,
PI Gerlach VL, Taupier RJ, Gusev VV, Coleman SD, Wolenc AR, Pena CEA,
XX Furtak K, Grose WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE,
XX
XX WPI, 2002-706998/76.

DR N-PSDB; AD116603.
XX
XX New NOVX polypeptides and nucleic acids, useful for preventing or
FT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
XX pharmacogenomics.
XX
XX Claim 1; SEQ ID NO 140; 1498pp; English.
XX
XX This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytoskeletal, cardiac, anti-inflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antiaesthetic, nephroprotective, antiarthritic, hepatotropic,
CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
XX invention.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 243; DB 5; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DVASRYAVODAPPEPAFTQAAHYLTYPENKAGTLYGQISADLDSP 48
DB 357 DVASRYAVODAPPEPAFTQAAHYLTYPENKAGTLYGQISADLDSP 404
RESULT 11
AD116606
ID AD116606 standard; protein; 781 AA.
AC
AC AD116606;
XX
DT 15-APR-2004 (first entry)
XX
DE Human NOVX protein to treat human pathological conditions segid142.
XX
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
KM inflammation; autoimmune disorder; allergy; blood disorder;
KM acquired immunodeficiency syndrome; AIDS; obesity; asthma;
KM immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
KM Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
KM cytoskeletal; cardiac; inflammation; immunosuppressive; antiallergic;
KM haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
KM antiaesthetic; nephroprotective; antiarthritic; hepatotropic;
KM neuroprotective; neurotropic; antibacterial; virucide; antiparasitic;
KM relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
KM chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
XX
XX WO200268649-A2.
XX

PD 06-SEP-2002.
 XX 31-JAN-2002; 2002W0-US002785.
 XX 31-JAN-2001; 2001US-0265395P.
 PR 31-JAN-2001; 2001US-0265412P.
 PR 31-JAN-2001; 2001US-0265514P.
 PR 31-JAN-2001; 2001US-0265517P.
 PR 02-FEB-2001; 2001US-0266406P.
 PR 05-FEB-2001; 2001US-0266767P.
 PR 07-FEB-2001; 2001US-0266975P.
 PR 08-FEB-2001; 2001US-0267057P.
 PR 09-FEB-2001; 2001US-0267459P.
 PR 15-FEB-2001; 2001US-0268974P.
 PR 26-FEB-2001; 2001US-0271664P.
 PR 27-FEB-2001; 2001US-0271839P.
 PR 02-MAR-2001; 2001US-0271855P.
 PR 02-MAR-2001; 2001US-0273046P.
 PR 14-MAR-2001; 2001US-0275925P.
 PR 14-MAR-2001; 2001US-0275947P.
 PR 14-MAR-2001; 2001US-0275950P.
 PR 14-MAR-2001; 2001US-0275989P.
 PR 15-MAR-2001; 2001US-0276448P.
 PR 15-MAR-2001; 2001US-0276450P.
 PR 16-MAR-2001; 2001US-0276397P.
 PR 16-MAR-2001; 2001US-0276568P.
 PR 20-MAR-2001; 2001US-0278652P.
 PR 26-MAR-2001; 2001US-0278775P.
 PR 26-MAR-2001; 2001US-0278778P.
 PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0279884P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282992P.
 PR 11-APR-2001; 2001US-0283083P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0286327P.
 PR 03-MAY-2001; 2001US-0286504P.
 PR 29-MAY-2001; 2001US-0294047P.
 PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296644P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0315447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 XX (CURA-) CURAGEN CORP.
 XX Tchernev VT, Spytek KA, Zernusen BD, Patturajan M, Shinkens RA;
 PI Li L, Gangolli EA, Padigara M, Anderson DM, Rastelli L, Miller CB;
 PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
 PI Fureak K, Grose WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 DR WPI; 2002-706998/76.
 DR N-PSDB; AD116605.
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX Claim 1; SEQ ID NO 142; 1498bp; English.
 PS
 XX This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytoskeletal, cardiac, anti-inflammatory, immunosuppressive, anti-allergic,
 CC hemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
 CC antistimatic, nephroprotective, antidiarrhetic, hepatoprotective,
 CC neuroprotective, neurotropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a human NOVX protein of the
 CC invention.
 XX
 XX Sequence 781 AA;
 SQ
 Query Match 100.0%; Score 243; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVASVRVANQDAPEPPAFQAAHYHTVPENKAPGTLVGCISAAADLSP 48
 Db 357 DVASVRVAQDAPEPPAFQAAHYHTVPENKAPGTLVQISAAADLSP 404
 |||||
 RESULT 12
 ID ABR40114 standard; protein; 781 AA.
 XX
 XX ABR40114;
 AC
 XX
 XX 04-JUL-2003 (first entry)
 DT
 XX
 XX Human cell adhesion and extracellular matrix protein, CADEC11.
 DE
 XX Human; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian;
 KW anticonvulsant; neuroprotective; immunosuppressive;
 KW dermatological; anti-inflammatory; cytoskeletal; antiatherosclerotic;
 KW Gene therapy; cell adhesion; extracellular matrix; CADEC1;
 KW Immune system disorder; AIDS; allergy; neurological disorder; stroke;
 KW Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
 KW cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
 KW genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
 KW atherosclerosis.
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO2003027230-A2.
 PN
 XX
 XX 03-APR-2003.
 PD
 XX
 XX 02-AUG-2002; 2002W0-US024649.
 PF
 XX
 XX 03-AUG-2001; 2001US-0309964P.
 PR 03-AUG-2001; 2001US-0310119P.
 PR 17-AUG-2001; 2001US-0315091P.
 PR 31-AUG-2001; 2001US-0316771P.

PR 07-SEP-2001; 2001US-0317896P.
 PR 21-SEP-2001; 2001US-0324781P.
 PR 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0381291P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
 PI Forsythe J, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
 PI Wallack DA, Xu Y, Honchell CD, Baughn MR, Gietzen KJ, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar U;
 XX
 DR WPI: 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 PS Claim 1, Page 192-194, 234pp; English.
 XX
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 XX
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 243; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVASVRVAVQDAPPEPAFTQAAVHLTPENKAPGTLVGQISADLDSF 48
 DB 357 DVASVRVAVQDAPPEPAFTQAAVHLTPENKAPGTLVGQISADLDSF 404
 RESULT 13
 ADA01366
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; antiinflammatory; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 PR 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI: 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 XX
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 243; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVASVRVAVQDAPPEPAFTQAAVHLTPENKAPGTLVGQISADLDSF 48
 DB 357 DVASVRVAVQDAPPEPAFTQAAVHLTPENKAPGTLVGQISADLDSF 404
 RESULT 14
 ADA43795
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003064474-A1.
 XX
 PD 03-APR-2003.

PF 16-SEP-2002; 2002US-00245859.
XX 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX MPI; 2003-605867/57.
DR N-Psdb; ADA43794.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 11; Fig 98; 308pp; English.
XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 243; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DVASRVAVVQDAPEPPAFQTAAYHLTVENKAPGTLVQGISADIDSP 48
DB 357 DVASRVAVVQDAPEPPAFQTAAYHLTVENKAPGTLVQGISADIDSP 404
RESULT 15
ADA43563
ADA43563 standard; protein; 781 AA.
XX
XX ADA43563;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human secreted/transmembrane polypeptide PRO34009.
DS

XX Human, PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2003073196-A1.
PN
XX
XX 17-APR-2003.
PD
XX
XX 18-SEP-2002; 2002US-00245210.
PF
XX
XX 04-APR-2001; 2001US-0282199P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
PI Fong S;
XX MPI; 2003-743814/70.
DR N-Psdb; ADA43562.
XX
PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT PRO21383 useful for stimulating the proliferation or differentiation of
PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 243; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 1,1e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Dec 8 11:46:23 2004

us-09-788-051-13.rag

Page 11

QY 1 DVASVRVAVQDAPEPPPAFTQAYHLLTPENKAPGTLVGQISADLDSP 48

DB 357 DVASVRVAVQDAPEPPPAFTQAYHLLTPENKAPGTLVGQISADLDSP 404

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Search completed: December 8, 2004, 10:13:06
Job time : 19.863 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 49.0484 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243
Sequence: 1 DVASRVAVQDAPEPPAFTQ.....ENKAPGTVGQISADLDSP 48

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	243	100.0	193	US-09-788-051-15
3	243	100.0	493	US-10-072-012-482
4	243	100.0	607	US-10-258-951-74
5	243	100.0	620	US-09-788-051-7
6	243	100.0	636	US-09-788-051-4
7	243	100.0	781	US-09-860-868-2
8	243	100.0	781	US-10-245-752-98
9	243	100.0	781	US-10-245-859-98
10	243	100.0	781	US-10-245-103-98
11	243	100.0	781	US-10-245-107-98
12	243	100.0	781	US-10-245-143-98
13	243	100.0	781	US-10-245-771-98

14	243	100.0	781	US-10-245-851-98	Sequence 98, Appl
15	243	100.0	781	US-10-245-883-98	Sequence 98, Appl
16	243	100.0	781	US-10-237-535-98	Sequence 98, Appl
17	243	100.0	781	US-10-238-183-98	Sequence 98, Appl
18	243	100.0	781	US-10-238-283-98	Sequence 98, Appl
19	243	100.0	781	US-10-238-370-98	Sequence 98, Appl
20	243	100.0	781	US-10-245-055-98	Sequence 98, Appl
21	243	100.0	781	US-10-245-147-98	Sequence 98, Appl
22	243	100.0	781	US-10-245-730-98	Sequence 98, Appl
23	243	100.0	781	US-10-245-739-98	Sequence 98, Appl
24	243	100.0	781	US-10-246-210-98	Sequence 98, Appl
25	243	100.0	781	US-10-239-196-98	Sequence 98, Appl
26	243	100.0	781	US-10-243-024-98	Sequence 98, Appl
27	243	100.0	781	US-10-243-409-98	Sequence 98, Appl
28	243	100.0	781	US-10-245-621-98	Sequence 98, Appl
29	243	100.0	781	US-10-245-880-98	Sequence 98, Appl
30	243	100.0	781	US-10-245-033-98	Sequence 98, Appl
31	243	100.0	781	US-10-243-095-98	Sequence 98, Appl
32	243	100.0	781	US-10-245-185-98	Sequence 98, Appl
33	243	100.0	781	US-10-245-427-98	Sequence 98, Appl
34	243	100.0	781	US-10-245-473-98	Sequence 98, Appl
35	243	100.0	781	US-10-245-770-98	Sequence 98, Appl
36	243	100.0	781	US-10-245-877-98	Sequence 98, Appl
37	243	100.0	781	US-10-246-976-98	Sequence 98, Appl
38	243	100.0	781	US-10-243-320-98	Sequence 98, Appl
39	243	100.0	781	US-10-162-435-13	Sequence 98, Appl
40	243	100.0	781	US-10-242-743-98	Sequence 98, Appl
41	243	100.0	781	US-10-242-845-98	Sequence 98, Appl
42	243	100.0	781	US-10-237-636-98	Sequence 98, Appl
43	243	100.0	781	US-10-238-325-98	Sequence 98, Appl
44	243	100.0	781	US-10-238-346-98	Sequence 98, Appl
45	243	100.0	781	US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-13
Sequence 13, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, X. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dimaec, Radoje T
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: HVS-39
CURRENT APPLICATION NUMBER: US/09/788,051
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-13

Query Match 100.0%; Score 243; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 3e-24;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DVASRVAVQDAPEPPAFTQAAYHLTVENKAPGTVGQISADLDSP 48

Db 1 DVASVRVAVQDAPPEPAFTQAAVHLLTPENKAPGTLVGQISAADLDSF 48

RESULT 2

US-09-788-051-15
Sequence 15, Application US/09788051
Publication No. US20030144491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenhua
APPLICANT: Drmanac, Radjoe T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: HXS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-15

Query Match

Best Local Similarity 100.0%; Score 243; DB 10; Length 193;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 96 DVASVRVAVQDAPPEPAFTQAAVHLLTPENKAPGTLVGQISAADLDSF 143

RESULT 3

US-10-072-012-482
Sequence 482, Application US/10072012
Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zehusen, Bryan
APPLICANT: Patruzjan, Meera
APPLICANT: Shimbets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esha
APPLICANT: Padigaru, Muraidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastrelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A.
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsbrock II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR FILING DATE: 2001-02-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 482

LENGTH: 493

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-482

Query Match

Best Local Similarity 100.0%; Score 243; DB 15; Length 493;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 357 DVASVRVAVQDAPPEPAFTQAAVHLLTPENKAPGTLVGQISAADLDSF 404

RESULT 4

US-10-258-951-74
Sequence 74, Application US/10258951
Publication No. US20040033504A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Khabick, Karen
APPLICANT: Lai, Ying-Ta
APPLICANT: Xie, Qing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50025
CURRENT APPLICATION NUMBER: US/10/258,951
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/13360
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,963
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/203,336
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/207,087
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,546
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-258-951-74

Query Match 100.0%; Score 243; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 6.5e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 357 DVASVRAVQDAPEPPAFTQAAYHLTPENKAPGTLVGQISADLDSF 404

RESULT 5
US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Alterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimaac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

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Best Local Similarity 100.0%; Pred. No. 5.7e-23;
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Db 341 DVASVRAVQDAPEPPAFTQAAYHLTPENKAPGTLVGQISADLDSF 388

RESULT 6
US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US20030144491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Alterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimaac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
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; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

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Db 357 DVASVRAVQDAPEPPAFTQAAYHLTPENKAPGTLVGQISADLDSF 404

RESULT 7
US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 57805, A NOVEL HUMAN CADHERIN FAMILY
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-868-2

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Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 357 DVASVRAVQDAPEPPAFTQAAYHLTPENKAPGTLVGQISADLDSF 404

RESULT 8
US-10-245-752-98
; Sequence 98, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C66
; CURRENT APPLICATION NUMBER: US/10/245,752
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24

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/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-752-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPPEPFTQAAYHLLTPENKAPGTLVQISADLDSF 48
DB 357 DVASRVAVQDAPPEPFTQAAYHLLTPENKAPGTLVQISADLDSF 404

RESULT 9
US-10-245-859-98
/ Sequence 98, Application US/10245859
/ Publication No. US20030064474a1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Bacon, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guirney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C78
/ CURRENT APPLICATION NUMBER: US/10/245, 859
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
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/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-859-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPPEPFTQAAYHLLTPENKAPGTLVQISADLDSF 48
DB 357 DVASRVAVQDAPPEPFTQAAYHLLTPENKAPGTLVQISADLDSF 404

RESULT 10
US-10-245-103-98
/ Sequence 98, Application US/10245103
/ Publication No. US20030068778A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Bacon, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Guirney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watanabe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C112
/ CURRENT APPLICATION NUMBER: US/10/245, 103
/ CURRENT FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-103-98

Query Match          100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPPEPFTQAAYHLLTPENKAPGTLVQISADLDSF 48
DB 357 DVASRVAVQDAPPEPFTQAAYHLLTPENKAPGTLVQISADLDSF 404
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Db 357 DVASVRVAVODAPEPPAFTOAAVHLTVPENKAPGTLVGOISADLDSF 404

RESULT 11

US-10-245-107-98
; Sequence 98, Application US/10245107
; Publication No. US2003006879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTOAAVHLTVPENKAPGTLVGOISADLDSF 48
Db 357 DVASVRVAVODAPEPPAFTOAAVHLTVPENKAPGTLVGOISADLDSF 404

RESULT 12

US-10-245-143-98
; Sequence 98, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin

APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-143-98

Query Match 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTOAAVHLTVPENKAPGTLVGOISADLDSF 48
Db 357 DVASVRVAVODAPEPPAFTOAAVHLTVPENKAPGTLVGOISADLDSF 404

RESULT 13

US-10-245-771-98
; Sequence 98, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114

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/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-771-98
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Query Match 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQGISADLIDSP 48
Db 357 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQGISADLIDSP 404
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RESULT 14
US-10-245-851-98
/ Sequence 98, Application US/10245851
/ Publication No. US20030068782A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, U. Christopher
/ APPLICANT: Guirney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C93
/ CURRENT APPLICATION NUMBER: US/10/245,851
/ CURRENT FILING DATE: 2002-09-15
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
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/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-851-98
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Query Match 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQGISADLIDSP 48
Db 357 DVASRVAVQDAPEPPAFQAAYHLTPENKAPGTLVQGISADLIDSP 404
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RESULT 15
US-10-245-883-98
/ Sequence 98, Application US/10245883
/ Publication No. US20030068783A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Baton, Dan
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Grimaldi, U. Christopher
/ APPLICANT: Guirney, Austin
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe
/ APPLICANT: Watambe, Colin
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ APPLICANT: Fong, Sherman
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3630R1C70
/ CURRENT APPLICATION NUMBER: US/10/245,883
/ CURRENT FILING DATE: 2002-09-15
/ PRIOR APPLICATION NUMBER: 10/197942
/ PRIOR FILING DATE: 2002-07-18
/ PRIOR APPLICATION NUMBER: 60/059114
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/063046
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/065027
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 60/079689
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: 60/086478
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: 60/087607
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: 60/089801
/ PRIOR FILING DATE: 1998-06-18
/ PRIOR APPLICATION NUMBER: 60/090557
/ PRIOR FILING DATE: 1998-06-24
/ PRIOR APPLICATION NUMBER: 60/090689
/ PRIOR FILING DATE: 1998-06-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 116
/ SEQ ID NO 98
/ LENGTH: 781
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-245-883-98
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Query Match 100.0%; Score 243; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 8,8e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Wed Dec 8 11:46:24 2004

us-09-788-051-13.rapb

Page 7

Cy 1 DVASVRAVODAPPEPPAFTQAAYH.LTVPENKAPGTLVGQISADLIDSP 48
Db 357 DVASVRAVODAPPEPPAFTQAAYH.LTVPENKAPGTLVGQISADLIDSP 404

Search completed: December 8, 2004, 11:34:30
Job time : 50.0484 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 5.72373 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-13

Perfect score: 243

Sequence: 1 DVASRYVAVQDAPRRPPTQ.....ENKAPGTLVQISADLDP 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478:39 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/prodata/1/aa/5A.COMB.pep:*
3: /cgn2_6/prodata/1/aa/5B.COMB.pep:*
4: /cgn2_6/prodata/1/aa/6A.COMB.pep:*
5: /cgn2_6/prodata/1/aa/6B.COMB.pep:*
6: /cgn2_6/prodata/1/aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	46.1	532	1	US-08-188-228-44 Sequence 44, Appl
2	112	46.1	532	1	US-08-332-638-44 Sequence 44, Appl
3	112	46.1	793	1	US-08-188-228-54 Sequence 54, Appl
4	112	46.1	793	1	US-08-332-643-48 Sequence 48, Appl
5	112	46.1	793	1	US-08-332-638-54 Sequence 54, Appl
6	112	46.1	799	1	US-08-188-228-42 Sequence 42, Appl
7	112	46.1	799	1	US-08-332-638-42 Sequence 42, Appl
8	111	45.7	693	4	US-08-738-349-6 Sequence 6, Appl
9	111	45.7	693	4	US-09-819-497-55 Sequence 55, Appl
10	111	45.7	796	2	US-08-738-349-4 Sequence 4, Appl
11	108	44.4	796	1	US-08-188-228-58 Sequence 58, Appl
12	108	44.4	796	1	US-08-332-643-52 Sequence 52, Appl
13	108	44.4	796	1	US-08-332-638-58 Sequence 58, Appl
14	108	44.4	796	2	US-08-738-349-2 Sequence 2, Appl
15	108	44.4	796	4	US-09-654-328-2 Sequence 2, Appl
16	106	43.6	794	1	US-08-188-228-60 Sequence 60, Appl
17	106	43.6	794	1	US-08-332-643-54 Sequence 54, Appl
18	106	43.6	794	1	US-08-332-638-60 Sequence 60, Appl
19	97	39.9	653	1	US-08-188-228-46 Sequence 46, Appl
20	97	39.9	653	1	US-08-332-638-46 Sequence 46, Appl
21	96.5	38.5	615	2	US-08-738-349-12 Sequence 12, Appl
22	93.5	38.5	787	1	US-08-453-695A-110 Sequence 110, Appl
23	93.5	38.5	787	1	US-08-268-161A-110 Sequence 110, Appl
24	93.5	38.5	787	3	US-08-453-702A-110 Sequence 110, Appl
25	93.5	38.5	787	3	US-09-099-639-110 Sequence 110, Appl
26	93.5	38.5	787	5	PCT-US95-08071-110 Sequence 110, Appl
27	88.5	36.4	743	4	US-09-489-847-168 Sequence 168, App

28	88.5	36.4	1026	1	US-07-998-003A-95	Sequence 95, Appl
29	88.5	36.4	1026	1	US-08-453-774E-95	Sequence 95, Appl
30	88.5	36.4	1026	1	US-08-453-695A-95	Sequence 95, Appl
31	88.5	36.4	1026	1	US-08-268-161A-95	Sequence 95, Appl
32	88.5	36.4	1026	2	US-08-453-702A-95	Sequence 95, Appl
33	88.5	36.4	1026	2	US-09-099-639-95	Sequence 95, Appl
34	88.5	36.4	1026	5	PCT-US93-12588-95	Sequence 95, Appl
35	88.5	36.4	1026	5	PCT-US95-08071-95	Sequence 95, Appl
36	88.5	36.4	1203	1	US-07-998-003A-103	Sequence 103, App
37	88.5	36.4	1203	1	US-08-453-274E-103	Sequence 103, App
38	88.5	36.4	1203	1	US-08-453-695A-103	Sequence 103, App
39	88.5	36.4	1203	1	US-08-268-161A-103	Sequence 103, App
40	88.5	36.4	1203	2	US-08-453-702A-103	Sequence 103, App
41	88.5	36.4	1203	3	US-09-099-639-103	Sequence 103, App
42	88.5	36.4	1203	5	PCT-US93-12588-103	Sequence 103, App
43	88.5	36.4	1203	5	PCT-US95-08071-103	Sequence 103, App
44	87.5	36.0	797	1	US-08-453-695A-112	Sequence 112, App
45	87.5	36.0	797	1	US-08-268-161A-112	Sequence 112, App

ALIGNMENTS

RESULT 1
US-08-188-228-44
Sequence 44, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shinfaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44
Query Match 46.1%; Score 112; DB 1; Length 532;
Best Local Similarity 45.7%; Pred. No. 2e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0;

ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 46.1%; Score 112; DB 1; Length 793;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTQAAYHUTVFNKAPGTLVGQISADLD 46
Db 367 DTATVXIVEDADEPVPFSSPTLLVFNHNAALNSVIGVATARDPD 412

RESULT 5
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 46.1%; Score 112; DB 1; Length 793;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;

Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTQAAYHUTVFNKAPGTLVGQISADLD 46
Db 367 DTATVXIVEDADEPVPFSSPTLLVFNHNAALNSVIGVATARDPD 412

RESULT 6
US-08-188-228-42
Sequence 42, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-42

Query Match 46.1%; Score 112; DB 1; Length 799;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy 1 DVASVRVAVODAPEPPAFTQAAYHUTVFNKAPGTLVGQISADLD 46
Db 374 DTATVXIVEDADEPVPFSSPTLLVFNHNAALNSVIGVATARDPD 419

RESULT 7
US-08-332-638-42
Sequence 42, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 125
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-42

Query Match 46.1%; Score 112; DB 1; Length 799;
Best Local Similarity 45.7%; Pred. No. 3.4e-07;
Matches 21; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPPEPAPFQAAYHILTPENKAPGTLVGQISAADLDS 46
DB 374 DTVTKIAYEDADEPMPFLAPSYIHEVQENNAAGTVGRVAKDPDA 419

RESULT 8
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Teujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 45.7%; Score 111; DB 2; Length 693;
Best Local Similarity 46.8%; Pred. No. 4e-07;
Matches 22; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPPEPAPFQAAYHILTPENKAPGTLVGQISAADLDS 47
DB 366 DTVTKIAYEDADEPMPFLAPSYIHEVQENNAAGTVGRVAKDPDA 412

RESULT 9
US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patent version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 45.7%; Score 111; DB 4; Length 693;
Best Local Similarity 46.8%; Pred. No. 4e-07;
Matches 22; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 DVASRVAVQDAPPEPAPFQAAYHILTPENKAPGTLVGQISAADLDS 47
DB 366 DTVTKIAYEDADEPMPFLAPSYIHEVQENNAAGTVGRVAKDPDA 412

RESULT 10
US-08-738-349-4
Sequence 4, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Teujimura, Atsushi
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; ADDRESSEE: Dunner
;; STREET: 1300 I Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/738,349
;; FILING DATE: 25-OCT-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/364,439
;; FILING DATE:
;; APPLICATION NUMBER: US 08/112,061
;; FILING DATE: 26-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barker, M. P.
;; REGISTRATION NUMBER: 32,013
;; REFERENCE/DOCKET NUMBER: 02481.1323-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 796 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-738-349-4
;;
;; Query Match 45.7%; Score 111; DB 2; Length 796;
;; Best Local Similarity 46.8%; Pred. No. 4.7e-07;
;; Matches 22; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
;;
;; QY 1 DVASRVAVQDAPEPPAFQTQAAYHLYTPENKAPGTLVGOISADLDS 47
;; DB 366 DVTWKIVSVDADPEPPMFLAPSYIHVQENNAAGTVGRVHAKDPDA 412
;;
;; RESULT 11
;; US-08-188-228-58
;; Sequence 58, Application US/08188228
;; Patent No. 559725
;; GENERAL INFORMATION:
;; APPLICANT: Suzuki, Shintaro
;; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
;; NUMBER OF SEQUENCES: 62
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Borun
;; STREET: 6300 Sears Tower, 233 S. Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/188,228
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/049,460

;;
;; FILING DATE: 19 APR 1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/872,643
;; FILING DATE: 17 APR 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 559725and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31340
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 796 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-188-228-58
;;
;; Query Match 44.4%; Score 108; DB 1; Length 796;
;; Best Local Similarity 44.7%; Pred. No. 1.3e-06;
;; Matches 21; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
;;
;; QY 1 DVASRVAVQDAPEPPAFQTQAAYHLYTPENKAPGTLVGOISADLDS 47
;; DB 366 DVTWKIVSVDADPEPPMFLAPSYIHVQENNAAGTVGRVHAKDPDA 412
;;
;; RESULT 12
;; US-08-332-643-52
;; Sequence 52, Application US/08332643
;; Patent No. 563634
;; GENERAL INFORMATION:
;; APPLICANT: Suzuki, Shintaro
;; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Bicknell
;; STREET: Two First National Plaza, 20 South Clark
;; STREET: Street
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60603
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/332,643
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/872,643
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 563634and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/30795
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 984-9740
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 52:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 796 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-332-643-52

Wed Dec 8 11:46:23 2004

us-09-788-051-13.ra1

Page 7

US-09-654-328-2

	Query Match	44.4%	Score 108	DB 4:	Length 796;
	Best Local Similarity	44.7%	Pred No. 13e-06;		
	Matches	21; Conservative	10; Mismatches	16; Indels	Gaps 0
Oy	1 DVASPRVADAPPEPFAFTQAAYHTVGENKAPGLTQICSAADS	47			
	: : : : : :				
Dd	366 DTVLTKRSVEDADEPPMLAEYSYHVEGNMAAGIVGAKNEDDA	412			

Search completed: December 8, 2004, 10:01:14
Job time : 5.72373 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.29398 seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-14
Perfect score: 82
Sequence: 1 VGTSVIQVTADADDP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	73	89.0	796 2	A38992 cadherin 11 precurs
2	73	89.0	796 2	I48277 cadherin-11 - mous
3	73	89.0	796 2	I49556 cadherin-11 - mous
4	73	89.0	796 2	A53584 OB-cadherin precurs
5	71	86.6	785 2	I50180 cadherin-7 - chick
6	67	81.7	790 2	G02678 Cadherin-14 - huma
7	67	81.7	790 2	I51638 F-cadherin - Afric
8	66	80.5	784 1	I0HUC5 cadherin 5 precurs
9	65	79.3	789 2	I52701 K-cadherin - rat
10	65	79.3	790 2	I50178 cadherin-6B - chic
11	65	79.3	790 2	I37016 cadherin-6 - human
12	59	72.0	793 2	D38992 cadherin 8 - human
13	56	68.3	712 1	I0USCT T-cadherin precurs
14	56	68.3	713 2	B38992 cadherin 13 precurs
15	56	68.3	717 2	I51206 T-cadherin 2 - chi
16	55	67.1	882 1	I0HUC6 cadherin 1 precurs
17	53	64.6	794 2	I59372 cadherin 12 - huma
18	53	64.6	822 1	I0USCP P-cadherin precurs
19	53	64.6	829 1	I0HUCP cadherin 3 precurs
20	52	63.4	877 1	I0BOCN N-cadherin precurs
21	52	63.4	906 1	I0HUCN cadherin 2 precurs
22	52	63.4	906 1	I0USCN N-cadherin precurs
23	52	63.4	912 1	I0CHCN gamma-aminobutyrat
24	50	61.0	484 1	F89908 E-cadherin precurs
25	50	61.0	884 1	I0USCE uvomocollin - mous
26	50	61.0	884 1	I0USCE uvomocollin - mous
27	50	61.0	4351 2	T00252 MEFP1 protein - ra
28	49	59.8	732 1	I0CHCB B-cadherin precurs
29	49	59.8	913 1	A47543 R-cadherin precurs

30	49	59.8	913 1	I0CHCR R-cadherin precurs
31	48	58.5	905 1	I0YLCL N-cadherin 1 precu
32	48	58.5	906 1	I0XLCL N-cadherin 2 precu
33	48	58.5	916 2	C38992 cadherin 4 precurs
34	47	57.3	458 2	AC1173 amino acid transpo
35	47	57.3	458 2	AD1530 amino acid transpo
36	47	57.3	770 2	B48910 desmocollin 1b pre
37	47	57.3	783 2	I50116 N-cadherin precurs
38	47	57.3	824 2	A48910 desmocollin 1a pre
39	47	57.3	840 2	I37281 Descln precursor -
40	47	57.3	887 1	I0CHCL Z-cadherin precurs
41	47	57.3	894 1	I37282 Dscib precursor -
42	47	57.3	2610 2	T20968 hypothetical prote
43	47	57.3	3034 2	T14119 seven-pass transme
44	46	56.1	761 1	I0BODE desmocollin 1a - b
45	46	56.1	809 1	I0BODD desmocollin 2b pre

ALIGNMENTS

RESULT 1

A38992
cadherin 11 precursor - human
N/Alternate names: OB-cadherin, osteoblast
C/Species: Homo sapiens (man)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: A38992
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A/Reference number: S24305; MIM:151283540; PMID:2059658
A/Accession: A38992
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <SUZ>
A/Cross-references: UNIPROT:P55287; GB:I34056; NID:G506403; PIND:AAA35622.1; PID:G50640
C/Genetics:
A/Genes: GDB:CDH11; OB
A/Cross-references: GDB:512891; OMIM:600023
C/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication
F/58-159/Domain: cadherin repeat homology <CR2>
F/162-268/Domain: cadherin repeat homology <CR3>
F/271-383/Domain: cadherin repeat homology <CR4>
F/386-488/Domain: cadherin repeat homology <CR4>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
Db 174 VGTSVIQVTADADDP 189

RESULT 2
I48277
cadherin-11 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48277
R/Hofmann, I.; Balling, R.
Dev. Biol. 169, 337-346, 1995
A/Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
A/Reference number: I48277; MIM:95269886; PMID:7750649
A/Accession: I48277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-796 <RES>
A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:G642796; PIND:CAA54674.1; PID:G666
C/Genetics:

A:Gene: cad-11
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADADDP 16
|||||
Db 174 VGTSTVIOVTADADDP 189

RESULT 3
149556

cadherin-11 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49556
R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Yeno, T.; Miyazaki, T.
Dev. Biol. 169, 347-358, 1995
A>Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
A:Reference number: I49556; MUID:96269897; PMID:7750650
A:Accession: I49556
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <R86>
A:Cross-references: UNIPROT:P55288; GB:D11963; NID:G974190; PIDN:BAA06730.1; PID:G974190
C:Superfamily: cadherin; cadherin repeat homology
F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADADDP 16
|||||
Db 174 VGTSTVIOVTADADDP 189

RESULT 4

OB-cadherin precursor - mouse
A:Species: Mus musculus (house mouse)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: A53584
R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Mann, E.
J. Biol. Chem. 269, 12092-12098, 1994
A>Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
A:Reference number: A53584; MUID:94216322; PMID:8163513
A:Accession: A53584
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796 <OKA>
A:Cross-references: UNIPROT:P55288; GB:D11253; NID:G994774; PIDN:BAA04797.1; PID:G994775
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: transmembrane protein
F:162-268/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:162-268/Domain: cadherin repeat homology <CR4>

Query Match 89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADADDP 16
|||||
Db 174 VGTSTVIOVTADADDP 189

RESULT 5
150180
cadherin-7 - chicken

C:Species: Gallus gallus (chicken)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I50180
R:Nakagawa, S.; Takeichi, M.
Development 121, 1321-1332, 1995
A>Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spec

A:Reference number: I50178; MUID:95509115; PMID:7540531
A:Accession: I50180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <NAK>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:G868000; PIDN:BAA07721.1; PID:G86800
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 86.6%; Score 71; DB 2; Length 785;
Best Local Similarity 87.5%; Pred. No. 0.00024;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADADDP 16
|||||
Db 168 VGTSTVIOVTADADDP 183

RESULT 6

cadherin-14 - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02678
R:Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01584
A:Accession: G02678
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <SHI>
A:Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:G1389852; PIDN:AB02933.1; PID:G1389852
C:Superfamily: cadherin; cadherin repeat homology
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 81.7%; Score 67; DB 2; Length 790;
Best Local Similarity 81.2%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADADDP 16
|||||
Db 174 VGTSTVIOVTADADDP 189

RESULT 7

F-cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51638; S55391
R:Espeseth, A.; Johnson, B.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A>Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mole
A:Reference number: I51638; MUID:96035533; PMID:7496627
A:Accession: I51638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ESP>
A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:G854634; PIDN:CAA59679.1; PID:G854634
C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 81.7%; Score 67; DB 2; Length 790;
Best Local Similarity 81.2%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSTVIOVTADADDP 16

Db 173 VGTSLVQVTAHDADDP 188

RESULT 8

10H0C5

cadherin 5 precursor - human

N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: S49893; S24305; A43418

R/Breviario: F.; Cavada, L.; Corada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp

submitted to the EMBL Data Library, June 1994

A/Description: Molecular and functional properties of VE-cadherin (7B4/cadherin-5) a nov

A/Reference number: S49893

A/Accession: S49893

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-784 <RES>

A/Cross-references: UNIPROT:P33151, EMBL:X79981, NID:G599833, PIDN:CAA56306.1, PID:G5998

R/Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A/Reference number: S24305; MUID:91283540; PMID:2059658

A/Accession: S24305

A/Molecule type: mRNA

A/Residues: 5-516, 'I', 518-784 <SUZ>

A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CAA42468.1; PID:G29593

R/Lampugnani, M.G.; Resnati, M.; Ralvert, M.; Pigott, R.; Pisacane, A.; Huen, G.; Ruco, J.

Cell Biol. 118, 1511-1522, 1992

A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts

A/Reference number: A43418; MUID:92394977; PMID:1522121

A/Accession: A43418

A/Molecule type: protein

A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254-

A/Experimental source: cultured endothelial cells

A/Note: Sequence extracted from NCBI Backbone (NCBIP:113040, NCBIP:113045, NCBIP:113047,

C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t

C/Genetics:

A/Gene: GDB:CDH5

A/Cross-references: GDB:134230; OMTM:601120

A/Map position: 16q22.1-16q22.1

C/Superfamily: cadherin; cadherin repeat homology

C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro

F:1-15/Domain: signal sequence #status predicted <SIG>

F:26-47/Domain: propeptide #status predicted <PRO>

F:48-784/Product: cadherin 5 #status predicted <MAT>

F:48-593/Domain: extracellular #status predicted <EXT>

F:50-151/Domain: cadherin repeat homology <CR1>

F:154-258/Domain: cadherin repeat homology <CR2>

F:261-372/Domain: cadherin repeat homology <CR3>

F:375-479/Domain: cadherin repeat homology <CR4>

F:481-587/Domain: cadherin repeat homology <CR5>

F:594-620/Domain: transmembrane #status predicted <TM>

F:621-784/Domain: intracellular #status predicted <INT>

F:736-753/Region: serine-rich

F:61, 112, 157, 362, 442, 523, 535/Binding site: carbohydrate (asn) (covalent) #status predict

Query Match 80.5%; Score 66; DB 1; Length 784;

Best Local Similarity 87.5%; Pred. No. 0.0019;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSLVQVTAHDADDP 16

Db 166 VGTSLVQVTAHDADDP 181

RESULT 9

152701

K-cadherin - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: I52701

R/Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igataashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, Cancer Res. 54, 3034-3041, 1994

A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer

A/Reference number: I52701; MUID:94243827; PMID:8187093

A/Accession: I52701

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-769 <RES>

A/Cross-references: UNIPROT:P55280, GB:D25290, NID:G435460, PIDN:BA04975.1, PID:G43546

C/Genetics:

A/Gene: KCAD

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity 79.3%; Score 65; DB 2; Length 789;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSLVQVTAHDADDP 16

Db 174 VGTSLVQVTAHDADDP 189

RESULT 10

150178

cadherin-6B - chicken

C/Species: Gallus gallus (chicken)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C/Accession: I50178

R/Nakagawa, S.; Takeichi, M.

Development 121, 1321-1332, 1995

A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe

A/Reference number: I50178; MUID:95309115; PMID:7540531

A/Accession: I50178

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-790 <NAK>

A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:G867998; PIDN:BA07720.1; PID:G86799

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 79.3%; Score 65; DB 2; Length 790;

Best Local Similarity 81.2%; Pred. No. 0.0029;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSLVQVTAHDADDP 16

Db 174 VGTSLVQVTAHDADDP 189

RESULT 11

137016

cadherin-6 - human

C/Species: Homo sapiens (man)

C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

C/Accession: I37016

R/Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirashashi, S.

Cancer Res. 55, 2206-2211, 1995

A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the

A/Reference number: I37016; MUID:95262134; PMID:7743525

A/Accession: I37016

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-790 <RES>

A/Cross-references: UNIPROT:P55285, GB:D31784; NID:G974184, PIDN:BA06562.1; PID:G97418

C/Genetics:

A/Gene: GDB:CDH6

C/Superfamily: cadherin; cadherin repeat homology

F:162-268/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity 79.3%; Score 65; DB 2; Length 790;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VGTSTVIOVTADHADDP 16
 |||:|||||
 Db 174 VGTFTVQVTATDADDP 169

RESULT 12

D38992

cadherin 8 - human

C:Species: Homo sapiens (man)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000

C:Accession: D38992

R:Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A:Reference number: S24305; MUID:91283540; PMID:2059658

A:Accession: D38992

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-793 <STU>

A:Cross-references: GB:L34060; NID:G506411; PIDN:AAA35628.1; PID:G506412

C:Genetics:

A:Gene: GDB:CDH8

A:Cross-references: GDB:5822911

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: calcium binding; cell adhesion; duplication

F:163-269/Domain: cadherin repeat homology <CDH>

Query Match

Best Local Similarity 72.0%; Score 59; DB 2; Length 793;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VGTSTVIOVTADHADDP 16
 |||:|||||
 Db 175 LGTSTVNTATDADDP 190

RESULT 13

IOMSC1

T-cadherin precursor - chicken

N:Alternate names: truncated cadherin

C:Species: Gallus gallus (chicken)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: U00279; S33272

R:Ranscht, B.; Douurs-Zimmermann, M.T.

Neuron 7, 391-402, 1991

A:Title: T-cadherin, a novel cadherin cell adhesion molecule in the nervous system lacks

A:Reference number: J00279; MUID:9200685; PMID:1654948

A:Accession: J00279

A:Molecule type: mRNA

A:Residues: 1-712 <RAN>

A:Cross-references: UNIPROT:P33150; GB:M61779; NID:G212708; PIDN:AAA49079.1; PID:G212709

A:Experimental source: embryonic brain

A:Note: part of this sequence, including the amino end of the mature protein, was confix

R:Cunningham, H.B.; Yazaki, P.O.; Domingo, R.C.; Oades, K.V.; Bohlen, H.; Sabbadini, R.A

Arch. Biochem. Biophys. 303, 32-43, 1993

A:Title: The skeletal muscle transverse tubular Mg-ATPase: identity with Mg-ATPases of s

A:Reference number: S33272; MUID:93255565; PMID:849284

A:Accession: S33272

A:Molecule type: protein

A:Residues: 139-153 <CON>

C:Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought b

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: blocked carboxyl end; calcium binding; cell adhesion; duplication; glycoprot

F:1-32/Domain: signal sequence #status predicted <SIG>

F:23-138/Domain: amino-terminal propeptide #status predicted <PRO>

F:139-693/Product: T-cadherin #status predicted <MAT>

F:141-245/Domain: cadherin repeat homology <CR1>

F:248-363/Domain: cadherin repeat homology <CR2>

F:366-477/Domain: cadherin repeat homology <CR3>

F:480-585/Domain: cadherin repeat homology <CR4>

F:566-691/Domain: cadherin repeat homology <CR5>

F:694-712/Domain: carboxyl-terminal propeptide #status predicted <CPR>

F:382,500,530,638,671/Binding site: carboxylate (Asn) (covalent) #status predicted

F:693/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form

Query Match

Best Local Similarity 68.3%; Score 56; DB 1; Length 712;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTSTVIOVTADHADDP 16
 |||:|||||
 Db 261 GTTVMRTAFDADDP 275

RESULT 14

B38992

cadherin 13 precursor - human

N:Alternate names: H-cadherin; T-cadherin

C:Species: Homo sapiens (man)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: B38992; G02676

R:Suzuki, S.; Sano, K.; Tanihara, H.

Cell Regul. 2, 261-270, 1991

A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t

A:Reference number: S24305; MUID:91283540; PMID:2059658

A:Accession: B38992

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-713 <STU>

A:Cross-references: UNIPROT:P55290; GB:L34058; NID:G506407; PIDN:AAA35624.1; PID:G506408

R:Lee, S.W.

submitted to the EMBL Data Library, May 1996

A:Reference number: H01582

A:Accession: G02676

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-713 <LEB>

A:Cross-references: EMBL:U59288; NID:G1381783; PIDN:AA18911.1; PID:G1381790

C:Genetics:

A:Gene: GDB:CDH13

A:Cross-references: GDB:5822917; OMIM:601364

C:Superfamily: cadherin; cadherin repeat homology

C:Keywords: blocked carboxyl end; calcium binding; cell adhesion; duplication; glycoprot

F:1-32/Domain: signal sequence #status predicted <SIG>

F:23-138/Domain: amino-terminal propeptide #status predicted <PRO>

F:141-245/Domain: cadherin repeat homology <CR1>

F:248-363/Domain: cadherin repeat homology <CR2>

F:366-477/Domain: cadherin repeat homology <CR3>

F:480-585/Domain: cadherin repeat homology <CR4>

F:586-691/Domain: cadherin repeat homology <CR5>

F:694-712/Domain: carboxyl-terminal propeptide #status predicted <CPR>

F:382,500,530,638,671/Binding site: carboxylate (Asn) (covalent) #status predicted

F:693/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match

Best Local Similarity 68.3%; Score 56; DB 2; Length 713;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTSTVIOVTADHADDP 16
 |||:|||||
 Db 261 GTTVMRTAFDADDP 275

RESULT 15

T-cadherin 2 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004

C:Accession: I51206

R:Sacristan, M.P.; Vestal, D.J.; Douurs-Zimmermann, M.T.; Ranscht, B.

J. Neurosci. Res. 34, 664-680, 1993

A:Title: T-cadherin 2: molecular characterization, function in cell adhesion, and coexpr

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A:Reference number: 151206; MUID:93301947; PMID:8315665
A:Accession: 151206
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-717 <SAC>
A:Cross-references: UNIPROT:P33150; GB:S62757; NID:G386362; PID:AA827242.1; PID:G386362
C:Superfamily: cadherin; cadherin repeat homology <CDH>
F:248-365/Domain: cadherin repeat homology <CDH>

Query Match          68.3%; Score 56; DB 2; Length 717;
Best Local Similarity 66.7%; Pred. NO. 0.1;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTSVIQVTAHDADDP 16
      ||:::|||
Db      261 GTTVMKMTAFDADDP 275

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Search completed: December 8, 2004, 10:27:08
Job time : 1.29398 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.41322 Seconds
(without alignments)

1435.471 Million cell updates/sec

Title: US-09-788-051-14

Perfect score: 82
Sequence: 1 VGTSVIQVTADADDP 16

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	100.0	241	2 Q6ET8	Q6ET8 homo sapien
2	82	100.0	493	2 Q96LQ7	Q96LQ7 homo sapien
3	82	100.0	781	2 Q6EFL6	Q6EFL6 mus musculu
4	82	100.0	781	2 AAH57373	AAH57373 mus muscu
5	82	100.0	819	1 CADO_HUMAN	Q8UPO6 homo sapien
6	73	89.0	792	1 CADB_CHICK	O9J319 gallus galli
7	73	89.0	794	2 O9J264	O9J264 xenopus lae
8	73	89.0	796	1 CADB_HUMAN	P55287 homo sapien
9	73	89.0	796	1 CADB_MOUSE	P55288 mus musculu
10	73	89.0	796	2 Q96CZ9	Q96CZ9 homo sapien
11	73	89.0	796	2 Q8C7Q6	Q8C7Q6 mus musculu
12	72	87.8	798	2 Q7ZYV7	Q7ZYV7 gallus galli
13	72	87.8	798	2 Q8QGH3	Q8QGH3 gallus galli
14	72	87.8	801	1 CADD_HUMAN	Q9H159 homo sapien
15	72	87.8	801	2 Q9ZDM3	Q9ZDM3 mus musculu
16	71	86.6	340	2 Q8BLT4	Q8BLT4 mus musculu
17	71	86.6	551	2 Q8AWM2	Q8AWM2 gallus galli
18	71	86.6	630	2 Q8LY78	Q8LY78 homo sapien
19	71	86.6	783	2 Q6TRK6	Q6TRK6 bos taurus
20	71	86.6	783	2 AAQ63484	AAQ63484 bos tauru
21	71	86.6	785	1 CADD_CHICK	Q9Q763 gallus galli
22	71	86.6	785	1 CADD_HUMAN	Q9H159 homo sapien
23	71	86.6	785	2 Q8BM52	Q8BM52 mus musculu
24	71	86.6	788	1 CADA_HUMAN	Q9Y6N8 homo sapien
25	71	86.6	788	2 Q8OWS7	Q8OWS7 mus musculu
26	71	86.6	788	2 Q8V168	Q8V168 mus musculu
27	71	86.6	788	2 AAH62962	AAH62962 mus muscu
28	71	86.6	789	1 CADA_CHICK	P79395 gallus galli
29	67	81.7	337	2 Q8BLT5	Q8BLT5 mus musculu
30	67	81.7	782	1 CADD_PIG	O02840 sus scrofa
31	67	81.7	782	2 Q8MWM5	Q8MWM5 sus scrofa

32	67	81.7	790	1 CADI_HUMAN	Q13634 homo sapien
33	67	81.7	790	2 Q8N522	Q8N522 homo sapien
34	67	81.7	790	2 Q91838	Q91838 xenopus lae
35	66	80.5	784	1 CADD_HUMAN	P31151 homo sapien
36	66	80.5	784	1 CADD_MOUSE	P55284 mus musculu
37	65	79.3	789	1 CADD_PAT	P55280 rattus norv
38	65	79.3	789	1 CADD_HUMAN	Q9A1B4 homo sapien
39	65	79.3	790	1 CADD_CHICK	Q9Q762 gallus galli
40	65	79.3	790	1 CADD_HUMAN	P55285 homo sapien
41	65	79.3	790	1 CADD_MOUSE	P97326 mus musculu
42	63	76.8	390	2 Q96KY9	Q96KY9 homo sapien
43	63	76.8	772	1 CADI_HUMAN	Q9H159 homo sapien
44	63	76.8	792	2 Q9DF50	Q9DF50 xenopus lae
45	63	76.8	792	2 Q9DF51	Q9DF51 xenopus lae

ALIGNMENTS

```
RESULT 1
Q6ET8      PRELIMINARY;      PRT;      241 AA.
ID  Q6ET8
AC  Q6ET8;
DT  01-JUN-2003 (Tremblrel. 24, Created)
DT  01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE  Full-length cDNA 5-PRIME end of clone CS00E010Y19 of Placenta of Homo
DE  sapiens (human) (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Placenta;
RA  Li W.B., Gruber C., Jessee J., Polayes D.;
RL  Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Placenta;
RA  Genoscope;
RL  Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- SIMILARITY: (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR  GO: GO:0016020; Cmembrane; IEA.
DR  GO: GO:0005509; F:calcium ion binding; IEA.
DR  GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR  InterPro: IPR002126; Cadherin.
DR  Pfam: PF00028; Cadherin; 2.
DR  PRINTS: PR00205; CADHERIN.
DR  SMART: SMC0112; CA; 2.
DR  PROSITE: PS00232; CADHERIN_1; 1.
DR  PROSITE: PS50268; CADHERIN_2; 2.
KW  Calcium; Calcium-binding.
FT  NON TER      241
FT  SEQUENCE     241 AA; 26348 MW; 4649831B55424604 CRC64;
SQ
Query Match      100.0%;      Score 82; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 366-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 2
Q96LQ7      PRELIMINARY;      PRT;      493 AA.
ID  Q96LQ7;
AC  Q96LQ7;
DT  01-DEC-2001 (Tremblrel. 19, Created)
DT  01-DEC-2001 (Tremblrel. 19, Last sequence update)
```

01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DT Hypothetical protein FLJ25193.
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Nishikawa K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Futaya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isega T., Sugano S.,
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; AK057922; BAB71613.1;
 DR HSSP; P12830; 1065.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016030; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; Cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 4.
 DR KAM; Calcium-binding.
 SQ SEQUENCE 493 AA; 53618 MW; 33F10DF63AF09C1E CRC64;
 Query Match 100.0%; Score 82; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGTSTVQTADADDP 16
 Db 165 VGTSTVQTADADDP 180
 ID Q6PFK6 PRELIMINARY; PRT; 781 AA.
 AC Q6PFK6;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Name=Cdh24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maiz M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependant cell adhesion proteins
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; BC057373; AAH57373.1;
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR00233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 DR KAM; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 781 AA; 84104 MW; 15996DE6C9835AA CRC64;
 Query Match 100.0%; Score 82; DB 2; Length 781;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGTSTVQTADADDP 16
 Db 165 VGTSTVQTADADDP 180
 ID AAH57373 PRELIMINARY; PRT; 781 AA.
 AC AAH57373;
 DT 02-MAR-2004 (Tremblrel. 27, Created)
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE Cadherin-like 24.
 GN Cdh24.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Maiz M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]


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RP SEQUENCEC FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC057373; AAH57373.1;
SQ SEQUENCE 781 AA; 84104 MM; 15996D6E6C935AA CRC64;

Query Match 100.0%; Score 82; DB 2; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSTVQTVAHDADDP 16
DB 165 VGTSTVQTVAHDADDP 180

RESULT 5
CADO_HUMAN STANDARD; PRT; 819 AA.
ID CADO_HUMAN STANDARD; PRT; 819 AA.
AC Q86UF0; Q86UPL; Q9N784;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-24 precursor (UNQ2834/PRO34009).
GN Name=CDH24; Synonyms=CDH11L;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
RP CATEINNS.
RX Medline=22753905; PubMed=12734196; DOI=10.1074/jbc.M304119200;
RA Kattafias B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
RT "Characterization of cadherin-24, a novel alternatively spliced type
RT II cadherin.";
RL J. Biol. Chem. 278:27513-27519(2003).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX Medline=228872296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Guney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chit C., Crowley C., Currell B., Denel B., Dowd P.,
RA Baton D., Foster J., Grimaldi L., Gu Q., Haas P.E., Helens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wleand Z., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood M.I.,
RA Gowdski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Testis;
RA Blum H., Baerends S., Mewes H.-N., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases
RL -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types. Cadherin-24 mediate strong
CC cell-cell adhesion.
CC -1- SUBUNIT: Associates with alpha-, beta- and delta-catenins.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Long form;
CC IsoId=Q86UF0-1; Sequence=displayed;
CC Name=2; Synonyms=Short form;
CC IsoId=Q86UF0-2; Sequence=VSP_008717;
CC Name=3;
CC IsoId=Q86UF0-3. Sequence=VSP_008718. VSP_008719;
CC

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CC CC Note=No experimental confirmation available;
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation at
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CC or send an email to license@isb-lib.ch).
CC -----
DR DR EMBL; AY260900; AAP205930.1; .
DR DR EMBL; AY260901; AAP20591.1; .
DR DR EMBL; AY358159; AAQ8856.1; .
DR DR EMBL; AL137477; CAB0758.1; .
DR DR PIR; T46418; T46418.
DR DR HSSP; P09803; 117W.
DR DR Genew; HGNC:14265; CDR24.
DR DR InterPro; IPR002126; Cadherin.
DR DR InterPro; IPR002233; Cadherin_C_term.
DR DR Pfam; PF00028; Cadherin_5.
DR DR Pfam; PF01049; Cadherin_C_1.
DR DR PRINTS; PR00205; CADHERIN.
DR DR PROSITE; PS00232; CADHERIN_1; 2.
DR DR PROSITE; PS50268; CADHERIN_2; 5.
KW KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
KW Multigene family; Repeat; Signal; Transmembrane.
FT FT SIGNAL 1 Potential.
FT FT PROPEP 19 Potential.
FT FT CHAIN 21 44 Cadherin-24.
FT FT TRANS 45 819 Extracellular (Potential).
FT FT DOMAIN 45 641 Potential.
FT FT TRANSMEM 642 662 Cytoplasmic (Potential).
FT FT DOMAIN 663 819 Cadherin 1.
FT FT DOMAIN 46 150 Cadherin 2.
FT FT DOMAIN 151 259 Cadherin 3.
FT FT DOMAIN 260 374 Cadherin 4.
FT FT DOMAIN 375 517 Cadherin 5.
FT FT DOMAIN 517 630 N-linked (GLNAC. . .) (Potential).
FT FT CARBOHYD 446 446 N-linked (GLNAC. . .) (Potential).
FT FT CARBOHYD 548 548 N-linked (GLNAC. . .) (Potential).
FT FT CARBOHYD 563 563 Missing (in isoform 2).
FT FT VASPLIC 455 492 /FtId-VSP 008717.
FT FT VASPLIC 1 427 Missing (in isoform 3).
FT FT VASPLIC 428 492 /FtId-VSP 008718.
FT FT VASPLIC EGTHITAFEDREARAHENLVLTATELGMSGNGPERGWPLL
FT FT VAWSAPAAPQRSPVGSAAVIPQ -> MNIVCTVCISHS
FT FT ALEFSTCTHAAYFMCFCLMLYASCIGHAAPHMFRVNCVCS
FT FT VMRCVFGLVP (in isoform 3).
FT FT /FtId-VSP 008719.
SQ SQ SEQUENCE 819 AA; 87751 MW; 9083034F18BATE4A CRC64;
Query Match 100.0%; Score 82; DB 1; Length 819;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy 1 VGTSVIQVTADADDP 16
Db 165 VGTSVIQVTADADDP 160
RESULT 6
CADB_CHICK STANDB.; PRT; 792 AA.
AC AC O9319;
DT DT 16-OCT-2001 (Rel. 40, Created)
DT DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DE Cadherin-11 precursor.
OS OS Name=Cadherin-11
OC OC Gallus gallus (Chicken).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
```

CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA Wei J., Dong X.R., Topouzis S., Zimmer W.E., Broders F., Thiery J.P.,
 RT "Molecular cloning of chick cadherin 11 and its expression during
 smooth muscle differentiation and formation of the tunica media";
 RT Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
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 CC or send an email to license@isb.ch).
 CC -----
 DR EMBL; AF055342; AAC3675.1; -
 DR HSP; P09803; 117W.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002123; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 53 Potential.
 FT CHAIN 54 792 Extracellular (Potential).
 FT DOMAIN 54 613 Extracellular (Potential).
 FT TRANSMEM 614 634 Potential.
 FT DOMAIN 635 792 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 608 Cadherin 5.
 FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 792 AA; 87572 MW; 3E3486C686731AB CRC64;
 QY
 Db 1 VGTSVIQTADADDP 16
 174 VGTSVIQTASDADDP 189
 Query Match 89.0%; Score 73; DB 1; Length 792;
 Best Local Similarity 93.8%; Pred. No. 0.0037;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OX Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Zygote;
 RA Hadeball B., Borchers A., Medlich D.;
 RT "Xenopus cadherin-11 (Xcadherin-11) expression requires the Wg/Wnt
 RT signal";
 RT Mech. Dev. 72:101-113 (1998).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AF002983; AAC28072.1; -
 DR HSP; P09803; 117W.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; P:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR002123; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS50268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Signal; Transmembrane.
 FT SIGNAL 1 53 Potential.
 FT CHAIN 54 794 cadherin.
 SQ SEQUENCE 794 AA; 88302 MW; 7221AD4CEA719DB CRC64;
 QY
 Db 1 VGTSVIQTADADDP 16
 174 VGTSVIQTASDADDP 189
 Query Match 89.0%; Score 73; DB 2; Length 794;
 Best Local Similarity 93.8%; Pred. No. 0.0037;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 ID CADB_HUMAN STANDARD; PRT; 796 AA.
 AC P55287; Q15065; Q15066; Q9U093; Q9U094;
 DT 01-OCT-1998 (Rel. 34, Created)
 DT 01-OCT-1998 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Heimerl R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin";
 RL Cell Adhes. Commun. 2:15-26 (1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amann B.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098 (1994).

```

RN [3]
RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=91283540; PubMed=2059658;
RA Suzuki S., Sano K., Tanihara H.;
RT "Diversity of the cadherin family: evidence for eight new cadherins in
  RT nervous tissue.";
RL Cell Regul. 2:261-270(1991).
RN [4]
RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
RA Koolis P.F.J., Hogendoorn P.C.M., Boyce J.V.M.G., Van Roy F.;
RT "Alternative cadherin-11 transcripts encoding truncated adhesion
  RT molecules are detectable in both human cancer and normal cells.";
  Submitted (ARR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
  CC They preferentially interact with themselves in a homophilic
  CC manner in connecting cells; cadherins may thus contribute to the
  CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
  CC Event=Alternative splicing; Named isoforms=2;
  CC Name=1;
  CC IsoId=P55287-1; Sequence=Displayed;
  CC Name=2;
  CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
  CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
  CC other tissues. Expressed in neuroblasts.
  CC -1- SIMILARITY: Contains 5 cadherin domains.
  CC -----
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  CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
  CC the European Bioinformatics Institute. There are no restrictions on its
  CC use by non-profit institutions as long as its content is in no way
  CC modified and this statement is not removed. Usage by and for commercial
  CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
  CC or send an email to license@isb-sib.ch).
  CC -----
  CC EMBL; L34056; AAA35622.1; -
  CC EMBL; D21254; BAA04798.1; -
  CC EMBL; D21255; BAA04799.1; -
  CC EMBL; AF060370; AAD27755.1; -
  CC EMBL; AF060368; AAD27755.1; JOINED.
  CC EMBL; AF060370; AAD27755.1; -
  CC EMBL; AF060369; AAD27755.1; JOINED.
  CC PIR; A38992; A38992.
  CC HSSP; P09803; 117M.
  CC Genew: HGNC:1750; CDH11.
  CC MIM; 600023; -
  CC GO; GO:0016021; C:integral to membrane; NAS.
  CC GO; GO:0007156; P:homophilic cell adhesion; NAS.
  CC GO; GO:0001503; P:osification; NAS.
  CC InterPro; IPR002126; Cadherin.
  CC InterPro; IPR000233; Cadherin_C_term.
  CC Pfam; PF000028; Cadherin; 5.
  CC Pfam; PF01049; Cadherin_C; 1.
  CC PRINTS; PR00205; CADHERIN.
  CC SMART; SM00112; CA; 5.
  CC PROSITE; PS00232; CADHERIN_1; 3.
  CC PROSITE; PS0268; CADHERIN_2; 5.
  CC KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
  KW Repeat; S-signal; Transmembrane.
  FT SIGNAL 1 22 Potential.
  FT PROPEP 23 53 Potential.
  FT CHAIN 54 796 Cadherin-11.
  FT DOMAIN 54 617 Extracellular (Potential).
  FT TRANSMEM 618 640 Potential.
  FT DOMAIN 641 796 Cytoplasmic (Potential).
  FT DOMAIN 54 159 Cadherin 1.
  FT DOMAIN 150 258 Cadherin 2.
  FT DOMAIN 259 383 Cadherin 3.
  FT DOMAIN 384 486 Cadherin 4.
  FT DOMAIN 487 612 Cadherin 5.
  FT CARBOHYD 455 455 N-linked (GlcNAc...) (Potential).

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FT	CABOBYD	540	540	N-linked (GlcNAc...)	(Potentially...)
FT	VASBPIC	632	693	51VLTAROKREPLIVEEDNENITLYDDEGGED	
FT	VASBPIC	632	693	TEADITLTONPDGINSFIR -> GCPSLMEPPSPEDMR	
FT	VASBPIC	632	693	LVIVGFLMPSYKVRKRFGLGVFLPLVIVVATESPT	
FT	VASBPIC	632	693	TLVSL (in isoform 2).	
FT	VASBPIC	632	693	/Ftrd=VSP 000640.	
FT	VASBPIC	632	693	Missing (in isoform 2).	
FT	VASBPIC	632	693	/Ftrd=VSP 000641.	
FT	VASBPIC	632	693	RL -> SV (in Ref. 2).	
FT	VASBPIC	632	693	M -> I (in Ref. 2).	
FT	VASBPIC	632	693	E -> K (in Ref. 2).	
FT	VASBPIC	632	693	S -> A (in Ref. 2).	
FT	VASBPIC	632	693	Q -> K (in Ref. 2).	
SO	SEQUENCE	796 AA;	88049 MM;	2C67044CT8ADBB32E CRC64;	
Query Match	Best Local Similarity	89.0%;	Score 73;	DB 1;	Length 796;
Matches	15; Conservative	93.8%;	Pred. No. 0.0037;		
		0; Mismatches	1;	Indels	0; Gaps
Oy	1	VGTSVIOVTADHADDP	16		
Db	174	VGTSVIOVTASDADDP	189		
RESULT 9					
CADB_MOUSE					
ID	CADB_MOUSE	STANDARD;	PRT;	796 AA.	
AC	P55288;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).				
GN	Name=Cdh11; Synonyms=Cad-11;				
OS	Musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=95269886; PubMed=7750649;				
RA	Hoffmann I.H., Balling R.;				
RT	"Cloning and expression analysis of a novel mesodermally expressed				
RT	cadherin.";				
RL	Dev. Biol. 169:337-346(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=95269887; PubMed=7750650;				
RA	Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,				
RA	Miyazaki T., Takeichi M.;				
RT	"Cadherin-11 expressed in association with mesenchymal morphogenesis				
RT	in the head, somite, and limb bud of early mouse embryos.";				
RL	Dev. Biol. 169:347-358(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=C57BL/6; TISSUE=Calvaria;				
RA	MEDLINE=94216322; PubMed=816313;				
RA	Okazaki M., Takehita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,				
RA	Amann E.;				
RT	"Molecular cloning and characterization of OB-cadherin, a new member				
RT	of cadherin family expressed in osteoblasts.";				
RL	J. Biol. Chem. 269:12092-12098(1994).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Olfactory epithelium;				
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,				
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditschke L., Marnins K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Franke C.,				
RA	Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				

FT	CABOBYD	455	455	N-linked (GlcNAc...)	(Potential)
FT	CABOBYD	540	540	N-linked (GlcNAc...) <td>(Potential)</td>	(Potential)
FT	CONFLICT	462	462	E -> D (in Ref. 1)	
FT	CONFLICT	589	589	T -> L (in Ref. 2)	
FT	CONFLICT	685	685	D -> N (in Ref. 2)	
FT	CONFLICT	751	751	V -> W (in Ref. 1)	
FT	CONFLICT	777	777	P -> Q (in Ref. 1)	
FT	CONFLICT	782	782	L -> P (in Ref. 2)	
SO	SEQUENCE	796 AA;	88112 MW;	0D584D24641DD529	CRC64;

Query Match	Best Local Similarity	93.8%	Score 73;	DB 1;	Length 796;
Matches 15;	Conservative	0;	Mismatches	1;	Indels 0;
					Gaps 0;

Qy	1	VGTSVIGVTADADDP	16
Db	174	VGTSVIGVTADADDP	189

RESULT 10	096C29	PRELIMINARY;	PRT;	796 AA.
ID	096C29			
AC	096C29			
DT	01-DEC-2001	(TEMBLrel. 19, Created)		
DT	01-DEC-2001	(TEMBLrel. 19, Last annotation update)		
DT	01-MAR-2004	(TEMBLrel. 26, Last annotation update)		
DE	Cadherin 11, type 2, isoform 1 preproprotein.			
GN	Name=CDH11;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buelow R.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,			
RA	Diatcchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schreier T.E.,			
RA	Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loguettano N.A., Peters G.U., Abramson R.D., Mulhaly S.J.,			
RA	Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunnaracne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzyzanski M.I., Skalska U., Smalusz D.E., Schmech A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Straussberg R.;			
RA	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins			
CC	(By similarity)			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).			
CC	-1- SIMILARITY: Contains 5 cadherin domains.			
DR	EMBL; BC013609; AAH13609.1; -			
DR	HSSP; P09803; 117M.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005509; P:calcium ion binding; IEA.			
DR	GO; GO:0007156; P:phospholipid cell adhesion; IEA.			
DR	InterPro; IPR002126; Cadherin.			
DR	InterPro; IPR00233; Cadherin_C_term.			
DR	InterPro; IPR001901; SecS.			

Query Match	89.0%;	Score 73;	DB 2;	Length 796;
Best Local Similarity	93.8%;	Pred. No. 0.0037;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps
Db	174	VGTSVQVTAHPADDP	189	
Oy	1	VGTSVQVTAHPADDP	16	
RESULT 11				
08C706				
ID	08C706	PRELIMINARY;	PRT;	796 AA.
AC	08C706;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, last annotation update)			
DE	Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length			
DE	enriched library, clone:CS30015P15 product:cadherin 11, full insert			
DE	sequence.			
GN	Name=cdh11;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Spinal cord;			
RC	MEDLINE=99279253; PubMed=10349636;			
RA	Carninci P., Hayashizaki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Math. Enzymol. 303:19-44(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Spinal cord;			
RC	MEDLINE=21085660; PubMed=11817851;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Spinal cord;			
RC	The FANTOM Consortium;			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RL	60,770 full-length cDNAs.";			
RN	Nature 420:563-573(2002).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Spinal cord;			
RC	MEDLINE=20493374; PubMed=11042159;			
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,			
RA	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,			
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to			
RL	prepare full-length cDNA libraries for rapid discovery of new genes.";			
RN	Genome Res. 10:1617-1630(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Spinal cord;			
RC	MEDLINE=20530913; PubMed=11076861;			
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,			
RA	Kono H., Akiyama J., Nishi K., Kitsuai T., Taahiro H., Itoh M.,			
RA	Sunai N., Ishi Y., Nakamura S., Hazama Y., Nishino T., Harada A.,			
RA	Yanamoto R., Matsunoto H., Sakaiguchi S., Ikegami T., Kasaiwagi K.,			

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RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai U.,
RA Okazaki Y., Mizumatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RC Adachi U., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirokane T.,
RA Horii F., Iwami K., Ichihara Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kamai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Niimi K., Nomura K., Numasaki R., Ono M., Ohashi N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sekizume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tasaga A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Yamamatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC CC -I- SIMILARITY: Contains 5 cadherin domains.
DR EMBL; AK049652; BAC3860.1; -.
DR HSSP; P09803; 117M.
DR MGD; MG1:99217; Cdhl1.
DR GO; GO:0005737; Cytoplasm; IDA.
DR GO; GO:0005866; Cytoplasmic membrane; IDA.
DR InterPro; IPRO01216; Cadherin.
DR InterPro; IPRO00233; Cadherin_C-term.
DR Pfam; PF00028; Cadherin_5; C-term.
DR Pfam; PF01049; Cadherin_C; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA_5
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR Calcium-binding; Cell adhesion; Transmembrane.
KW Caclium-binding; Cell adhesion; Transmembrane.
SQ SEQUENCE 796 AA; 88126 MW; 71963374B2E3BE29 CRC64;

Query Match      89.0%; Score 73; DB 2; Length 796;
Best local Similarity   93.8%; Pred. NO. 0.0037;
Matches    15; Conservative     0; Mismatches     1; Indels     0; Gaps     0.

QY          1 VGTSVIQVTADADDP 16
              |||||
Db           174 VGTSVIQVTASDADDP 189

RESULT 12
O7ZYV7       PRELIMINARY;      PRT;      798 AA.
ID QZYZV7;
CD 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE F-cadherin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic motor neuron;
RA Shitabe K., Kimura Y., Fukushima M., Matsuo N., Yoshioka H.,
RA Tanaka H.;
RL Submitted (JUN-2002) to the EMBL/Genbank/DDJ databases.
CC -I- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- SIMILARITY: Contains 3 cadherin domains.
```

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DR EMBL: AF465257; AAC3355.1; -.
DR HSSP: P09803; 117W.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 3.
DR PROSITE: PS50268; CADHERIN_2; 3.
DR Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 798 AA; 89156 MW; 8224F837937F106 CRC64;

Query Match      87.8%; Score 72; DB 2; Length 798;
Best Local Similarity 93.8%; Pred. No. 0.0054;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADADDP 16
   |||||
Db 179 VGTSVIQVTADADDP 194

RESULT 13
O8QGH3 PRELIMINARY; PRT; 798 AA.
ID O8QGH3
AC O8QGH3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mn-cadherin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Jessell T.M., Price S.R.;
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC -1- (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Contains 3 cadherin domains.
DR EMBL: AF459439; AAL93123.1; -.
DR HSSP: P09803; 117W.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS0268; CADHERIN_2; 3.
DR PROSITE: PS50268; CADHERIN_2; 3.
DR Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 798 AA; 89156 MW; 8224F837937F106 CRC64;

Query Match      87.8%; Score 72; DB 2; Length 798;
Best Local Similarity 93.8%; Pred. No. 0.0054;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 179 VGTSVIQVTADADDP 194

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ID CADC_HUMAN STANDARD; PRT; 801 AA.
AC Q9HBT6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cadherin-20 precursor.
GN Name=CDH20; Synonyms=CDH7L3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20453188; PubMed=10995570;
RA Koos P., Van Imschoot G., van Roy F.;
RT "Characterization of three novel human cadherin genes (CDH7, CDH19,
RT and CDH20) clustered on chromosome 18q22-q23 and with high homology to
RT chicken cadherin-7."
RL Genomics 68:283-295(2000).
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells; cadherins may thus contribute to the
CC sorting of heterogeneous cell types.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in placenta, adult brain, and fetal
CC brain.
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: AF217289; AAG3739.1; -.
DR HSSP: P09803; 117X.
DR Genew: HGNC:1760; CDH20.
DR MIM: 605807; -.
DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0007156; P:homophilic cell adhesion; NAS.
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_C-term.
DR Pfam: PF00028; Cadherin_5.
DR Pfam: PF01049; Cadherin_C_1.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA; 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS50268; CADHERIN_2; 5.
DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 ? Potential.
FT PROPEP 59 Potential.
FT CHAIN 60 801 Extracellular (Potential).
FT DOMAIN 1 619 Potential.
FT TRANSXEM 620 640 Cytoplasmic (Potential).
FT DOMAIN 641 801 Cadherin_1.
FT DOMAIN 161 165 Cadherin_2.
FT DOMAIN 166 274 Cadherin_3.
FT DOMAIN 275 389 Cadherin_4.
FT DOMAIN 390 494 Cadherin_5.
FT DOMAIN 494 610 Cadherin_5.
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 420 420 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 542 542 N-linked (GlcNAc...) (Potential).
KW SEQUENCE 801 AA; 89104 MW; FB5D353E163166 CRC64;

Query Match      87.8%; Score 72; DB 1; Length 801;
Best Local Similarity 93.8%; Pred. No. 0.0054;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 VGTSVIOVTADHADDP 16
 DB 180 VGTSVIOVTADHADDP 195

RESULT 15

Q9Z0M3 PRELIMINARY; PRT; 801 AA.

AC Q9Z0M3
 DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Cadherin 7 precursor (Mus musculus adult male diencephalon cDNA, RIKEN
 DE full-length enriched library, clone:9330198E05 product:cadherin 7,
 DE full insert sequence).
 GN Name=Cdh20; Synonyms=Cdh7;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

[1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss random bred; TISSUE=Eye;
 RX MEDLINE=99365480; PubMed=10433813;
 RA Faulkner-Jones B.E., Godinho U.N.M., Reese B.E., Pasquini G.F.,
 RA Ruefli A., Tan S.-S.;
 RT "Cloning and expression of mouse Cadherin-7, a type-II cadherin
 RT isolated from the developing eye.";
 RL Mol. Cell. Neurosci. 14:1-16(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=99279253; PubMed=10349366;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).
 [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Adachi T., Aizawa K., Akimura T., Aikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AF007116; AAD01278.1; -;
 DR EMBL; AK034475; BAC28721.1; -;
 DR HSSP; P09803; 117X.
 DR MGD; MG1:1346069; Cdh20.
 DR GO; GO:0016020; C-membrane;
 DR GO; GO:0005509; F-calcium ion binding; IEA.
 DR GO; GO:0007156; P-homophilic cell adhesion; IEA.
 DR DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin; 5.
 DR Pfam; PF01049; Cadherin_C; 1.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 DR KEGG; K04400; Cadherin; 5.
 FT SIGNAL 1 Potential.
 FT CHAIN 60 801 cadherin 7.
 SQ SEQUENCE 801 AA; 8897 MW; AECF5C7A2D6CFBC CRC64;

QY 1 VGTSVIOVTADHADDP 16
 DB 180 VGTSVIOVTADHADDP 195

Search completed: December 8, 2004, 10:24:40
 Job time : 6.41322 secs

Query Match 87.8%; Score 72; DB 2; Length 801;
 Best Local Similarity 93.8%; Pred. No. 0.0054;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 6.62102 Seconds
(without alignments)
866.886 Million cell updates/sec

Title: US-09-788-051-14

Perfect score: 82
Sequence: 1 VGTSVIQTAVHADDDP 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	16	7	ADD29455 Human cad
2	82	100.0	48	7	ADD29449 Human cad
3	82	100.0	493	5	AD116946 Human NOV
4	82	100.0	607	5	ABBS3295 Human pol
5	82	100.0	620	7	ADD29448 Human pol
6	82	100.0	636	7	ADD29445 Human cad
7	82	100.0	781	5	ABBS3296 Human pol
8	82	100.0	781	5	AAW48736 Human cad
9	82	100.0	781	5	ABG34078 Human pro
10	82	100.0	781	5	AD116604 Human NOV
11	82	100.0	781	5	AD116606 Human NOV
12	82	100.0	781	6	ABR40114 Human cel
13	82	100.0	781	6	ADA01366 Human pro
14	82	100.0	781	6	ADA43795 Human sec
15	82	100.0	781	6	ADA43563 Human sec
16	82	100.0	781	6	ADA01238 Human pro
17	82	100.0	781	6	ADA01122 Human sec
18	82	100.0	781	7	ADA43579 Human sec
19	82	100.0	781	7	ADA06941 Human pro
20	82	100.0	781	7	ADA08429 Human pro
21	82	100.0	781	7	ADB99722 Human hum
22	82	100.0	781	7	ADB87005 Human pro
23	82	100.0	781	7	ADB66160 Human pro
24	82	100.0	781	7	ADB99838 Human pro
25	82	100.0	781	7	ADB99493 Human hum

26	82	100.0	781	7	ADB66044 Human sec
27	82	100.0	781	7	ADC23442 Human tra
28	82	100.0	781	7	ADC26135 Human pro
29	82	100.0	781	7	ADE04962 Human pro
30	82	100.0	781	7	ADE11268 Human pro
31	82	100.0	781	7	ADB88199 Human pro
32	82	100.0	781	7	ADD95494 Human sec
33	82	100.0	781	7	ADE06424 Human pro
34	82	100.0	781	7	ADB38199 Human pro
35	82	100.0	781	7	ADB88315 Human pro
36	82	100.0	781	7	ADD90896 Human sec
37	82	100.0	781	7	ADP99451 Human sec
38	82	100.0	781	7	ADG06544 Human pro
39	82	100.0	781	7	ADG05495 Human pro
40	82	100.0	781	7	ADG82496 Human pro
41	82	100.0	781	8	ADRS1749 Human sec
42	82	100.0	781	8	ADE51865 Human sec
43	82	100.0	781	8	ADRS3723 Human sec
44	82	100.0	781	8	ADRS37607 Human sec
45	82	100.0	781	8	ADRS5378 Human sec

ALIGNMENTS

RESULT 1	
ADD29455	
ID ADD29455 standard; peptide, 16 AA.	
XX	
AC ADD29455;	
XX	
DT 15-JUN-2004 (first entry)	
XX	
DE Human cadherin-like protein peptide fragment Seq ID14.	
XX	
KW cadherin-like protein; transmembrane protein; cadherin domain;	
KW homotypic cell-cell adhesion; cytotactin; osteopontin; cancer;	
KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;	
KW metastatic tumour; human.	
XX	
OS Homo sapiens.	
XX	
PN US200314491-A1.	
XX	
PD 31-JUL-2003.	
XX	
PF 16-FEB-2001; 2001US-00786051.	
XX	
PR 03-FEB-2000; 2000US-00496914.	
PR 27-APR-2000; 2000US-00560875.	
XX	
PA (GODB/) GODBOLE S. D.	
PA (KUOC/) KUO C.	
PA (ARTE/) ARTERBURN M. C.	
PA (YEUN/) YEUNG G.	
PA (PALE/) PALENCIA S.	
PA (TANG/) TANG Y. T.	
PA (LIUC/) LIU C.	
PA (DRMA/) DRMANAC R. T.	
XX	
PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT;	
PI Liu C, Drmanac RT;	
XX	
DR WPI; 2003-829799/77.	
XX	
PT Novel isolated human secreted cadherin-like polypeptide useful for	
PT treating diseases such as cancers, osteoporosis, Paget's disease,	
PT osteomalacia, hyperostosis, osteopetrosis.	
XX	
PS Claim 11; SEQ ID NO 14; 63bp; English.	
XX	
CC This invention relates to a novel isolated human secreted cadherin-like	
CC protein and the DNA sequence which encodes it. Cadherins are a family of	

transmembrane proteins which share a common cadherin domain in their extracellular region. The extracellular portion mediates homotypic cell-cell adhesion. The cytoplasmic portion contains a conserved protein sequence which encodes it. Cadherins are a family of

PR 26-MAR-2001; 2001US-0278778P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P

29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282952P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313908P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318118P.
PR 07-SEP-2001; 2001US-0318748P.
PR 12-SEP-2001; 2001US-0323379P.
PR 19-SEP-2001; 2001US-0323745P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Tchernev VT, Szytek KA, Zernusen BD, Paturajan M, Shinkens PA;
PI Li L, Gangoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach VM, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grose WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
XX WPI; 2002-706998/76.
XX
XX New NOXV polypeptides and nucleic acids, useful for preventing or
PT treating NOXV-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Disclosure: SEQ ID NO 482; 1498pp; English.
PS
XX
XX This invention relates to a novel nucleic acid, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOXV proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOXV polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOXV-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiatherosclerotic, anorectic,
CC antihypertensive, nephroprotective, antiarthritic, hepatotropic,
CC neuroprotective, nocotropic, antibacterial, virucide, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a homologue of a human NOXV protein
CC of the invention.
XX
XX Sequence 493 AA;
SQ

Query Match

100.0%; Score 82; DB 5; Length 493;

Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGTSTVYQVTAHDADDP 16
DB 165 VGTSTVYQVTAHDADDP 180
RESULT 4
ID ABB53295
ID ABB53295 standard; protein; 607 AA.
AC ABB53295;
XX
XX 12-FEB-2002 (first entry)
XX
XX Human polypeptide #35.
DE
XX Human; nocrotropic; neuroprotective; anticonvulsant; antidepressant;
XX neuroleptic; tranquilliser; antiaxrhymic; cardiant; antiaesthetic;
XX antiinflammatory; antilipemic; hepatotropic; virucide; antidiabetic;
XX nephroprotective; anorectic; cyostatic; vaccine; neurological disease;
XX cardiovascular disease; respiratory disease; liver disease;
XX renal disease; skeletal muscle disease; gastrointestinal disease;
XX placental disease; testicular cancer; male fertility; pancreatic disease.
XX
XX Homo sapiens.
OS
XX
XX WO200181363-A1.
XX
XX 01-NOV-2001.
XX
XX 26-APR-2001; 2001WO-US013360.
XX
XX 27-APR-2000; 2000US-0199963P.
XX 11-MAY-2000; 2000US-0203336P.
XX 25-MAY-2000; 2000US-0207087P.
XX 26-MAY-2000; 2000US-0207546P.
XX
XX (SMIX) SMITHKLINE BEECHAM CORP.
XX (SMIX) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdock PR, Ravi SK, Smith RF, Xiang Z, Kahnick KS;
PI Lai Y, Xie Q;
XX
XX WPI; 2002-041392/05.
XX N-PSDB; ABA903360.
XX
XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
PT and treating diseases associated the polypeptide, e.g. Alzheimer's
PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
XX
XX Claim 1; Page 106-108; 116pp; English.
PS
XX
XX The invention relates to an isolated polypeptide comprising a 277, 480,
XX 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
XX 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
XX 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
XX given in the specification. The polypeptides, modulators of the
XX polypeptides and antibodies against the polypeptides are useful for
XX treating diseases such as neurological and psychiatric diseases including
XX Alzheimer's, paraneuronal palsy, Huntington's disease, myotonic
XX dystrophy, anorexia and depression; cardiovascular diseases including
XX congestive heart failure, Hodgkin's disease and myocardial infarction;
XX respiratory diseases including asthma, chronic obstructive pulmonary
XX disease, cystic fibrosis and adult respiratory distress syndrome; liver
XX diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
XX hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
XX renal disease including renal failure, acute tubular necrosis and
XX glomerulonephritis; skeletal muscle diseases including Duchenne's
XX disease, hypoglycaemia and obesity; gastrointestinal diseases including
XX myotonia congenita and intestinal obstruction; lymph diseases including
XX lymphagiectasia; diseases of placenta including choriocarcinoma; diseases

CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention
 XX

SQ Sequence 607 AA;

Query Match 100.0%; Score 82; DB 5; Length 607;
 Best Local Similarity 100.0%; Pred. No. 3,7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADHDDP 16
 |||||
 Db 165 VGTSVIQVTADHDDP 180

RESULT 5
 ADD29448
 ID ADD29448 standard; protein; 620 AA.

AC ADD29448;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;

KW homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.

OS Homo sapiens.

XX US2003144491-A1.

XX 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
 PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

XX Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 7; 63bp; English.

PS This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutic useful for the treatment of diseases

CC such as cancers, osteoporosis, Paget's disease, osteomalacia,

CC hyperostosis and osteopetrosis. The protein and DNA sequence of the

CC invention may also be useful as markers for prognosis of metastatic

CC tumours. The present sequence is that of the mature human secreted

CC cadherin-like protein which was used during the exemplification of the

CC invention.

XX Sequence 620 AA;

Query Match 100.0%; Score 82; DB 7; Length 620;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADHDDP 16
 |||||
 Db 149 VGTSVIQVTADHDDP 164

RESULT 6
 ADD29445
 ID ADD29445 standard; protein; 636 AA.

AC ADD29445;

DT 15-JAN-2004 (first entry)

DE Human cadherin-like protein amino acid sequence.

XX cadherin-like protein; transmembrane protein; cadherin domain;

KW homotypic cell-cell adhesion; cytosstatic; osteopathic; cancer;

KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.

OS Homo sapiens.

XX Key

XX Peptide

XX Protein

XX US2003144491-A1.

XX 31-JUL-2003.

PF 16-FEB-2001; 2001US-00788051.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PA (GODB/) GODBOLE S D.

PA (KUOC/) KUO C.

PA (ARTE/) ARTERBURN M C.

PA (YEUN/) YEUNG G.

PA (PALE/) PALENCIA S.

PA (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (DRMA/) DRMANAC R T.

PI Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YT,
 PI Liu C, Drmanac RT;

DR WPI; 2003-829799/77.

DR N-PSDB; ADD29461, ADD29446.

XX Novel isolated human secreted cadherin-like polypeptide useful for

PT treating diseases such as cancers, osteoporosis, Paget's disease,

PT osteomalacia, hyperostosis, osteopetrosis.

XX Claim 11; SEQ ID NO 4; 63bp; English.

PS This invention relates to a novel isolated human secreted cadherin-like

CC protein and the DNA sequence which encodes it. Cadherins are a family of

CC transmembrane proteins which share a common cadherin domain in their

CC extracellular region. The extracellular portion mediates homotypic cell-

CC cell adhesion that is calcium dependent. Modulators of the protein of the

CC invention may have cytostatic or osteopathic activity. The invention may

CC allow development of therapeutics useful for the treatment of diseases
 CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
 CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
 CC invention may also be useful as markers for prognosis of metastatic
 CC tumours. The present sequence is that of the human secreted cadherin-like
 CC protein of the invention.

CC Sequence 636 AA:

Query Match 100.0%; Score 82; DB 7; Length 636;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADHADDP 16
 |||||
 DB 165 VGTSVIQVTADHADDP 180

RESULT 7
 ID ABB53296
 AC ABB53296; protein, 781 AA.

DT 12-FEB-2002 (first entry)

DE Human polypeptide #36.

KM Human, noctropic; neuroprotective; anticonvulsant; antidepressant;
 KM neuroleptic; tranquiliser; antiarrhythmic; cardiant; antidiabetic;
 KM antiinflammatory; antihypertensive; hepatotropic; virucide; antidiabetic;
 KM nephrotoxic; anorectic; cytostatic; vaccine; neurological disease;
 KM cardiovascular disease; respiratory disease; liver disease;
 KM renal disease; skeletal muscle disease; gastrointestinal disease;
 KM placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

OS WO200181363-A1.

PN 01-NOV-2001.

PD 26-APR-2001; 2001WO-US013360.

PF 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

PA (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;

PI Lai Y, Xie Q;

PT Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesias.

PS Claim 1; Page 108-109; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 584, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026,
 CC 784, 785, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraupranuclear palsy, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression, cardiovascular diseases including

CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolaemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, and impaired glucose tolerance;
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Rulenburg's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphoglandular diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

CC Sequence 781 AA:

Query Match 100.0%; Score 82; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADHADDP 16
 |||||
 DB 165 VGTSVIQVTADHADDP 180

RESULT 8
 ID AAM48736
 AC AAM48736; protein, 781 AA.

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

KM Human, cadherin 57805; osteopathic; hepatotropic; antibacterial;
 KM antidiabetic; neuroprotective; antiarrhythmic; antineumatic;
 KM dermatological; immunosuppressive; antiinflammatory; antipruritic;
 KM antihypertensive; antidiabetic; antileptotic; haemostatic; antidiabetic;
 KM anorectic; immunomodulatory; vasoregulatory; virucide; antidiabetic;
 KM thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 KM viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 KM osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 KM thrombus; inflammation; infection; ischaemia; irritable bowel syndrome;
 KM gene therapy.

XX Homo sapiens.

OS WO200190145-A2.

PN 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Curtis RAJ;

PT WPI: 2002-083082/11.
 N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for
 PT diagnosing and treating disorders e.g. obstructive jaundice, multiple
 PT sclerosis, encephalomyelitis and atherosclerosis and to identify
 PT modulators of therapeutic use.
 PS Claim 9; Page 105; 119pp; English.
 XX The invention relates to human cadherin family polypeptide designated

CC 57805 with osteopathic, hepatotropic, antibacterial, antidiabetic,
 CC neuroprotective, antiarrhythmic, antineumatic, dermatological,
 CC immunosuppressive, antineoplastic, antiparasitic, antisthmatic,
 CC antiallergic, antileptotic, haemostatic, antipruritic, antihypertensive,
 CC antineoplastic, antineoplastic, antineoplastic, antineoplastic,
 CC immunomodulatory, vasorelaxant, cardiotonic, antineoplastic, anorectic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy, cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
 CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis; viral diseases; metabolic or pain disorders
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy

CC XX
 CC SQ Sequence 781 AA;

Query Match 100.0%; Score 82; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSTVIGTADADDP 16
 |||||
 DB 165 VGTSTVIGTADADDP 180

RESULT 9
 ABG34078 standard; protein: 781 AA.

AC ABG34078;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 XX
 DE Human Pro peptide #49.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; Cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO200224888-A2.
 PN
 XX
 XX 28-MAR-2002.
 PD
 XX
 XX 29-AUG-2001; 2001WO-US027099.
 PF
 XX
 XX 01-SEP-2000; 2000US-0229896P.
 PR 05-SEP-2000; 2000US-0230621P.
 PR 22-SEP-2000; 2000US-0235147P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 25-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264385P.
 PR 02-FEB-2001; 2001US-0264421P.
 PR 09-FEB-2001; 2001US-0267632P.
 PR 28-FEB-2001; 2001WO-US06520P.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282129P.
 PR 09-MAY-2001; 2001US-0280589P.
 PR 23-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 XX
 XX (GENT) GENENTECH INC.
 PA
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 XX WPI; 2002-362426/39.
 DR N-PSDB; ABK70009.
 XX
 XX
 PT New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or for
 PT genetic analysis of individuals with genetic disorders.
 PT
 PT Claim 11, Fig 98; 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. Polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention

CC XX
 CC SQ Sequence 781 AA;

Query Match 100.0%; Score 82; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VGTSTVIGTADADDP 16
 |||||
 DB 165 VGTSTVIGTADADDP 180

RESULT 10
 AD116604 standard; protein: 781 AA.

AC AD116604;
 XX
 XX 15-APR-2004 (first entry)
 DT
 XX
 DE Human NOVX protein to treat human pathological conditions segid140.
 XX
 XX
 KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytostatic; cardiant; antineoplastic; immunosuppressive; antiallergic;
 KW haemostatic; anti-HIV; antidiabetic; antineoplastic; anorectic;
 KW antineoplastic; nephrotropic; antineoplastic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
 KW single nucleotide polymorphism.

XX Homo sapiens.
OS
XX WC200268649-A2.
XX
PD 06-SEP-2002.
XX
PF 31-JAN-2002; 2002W0-US002785.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267453P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0276552P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0278882P.
PR 29-MAR-2001; 2001US-0278884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282952P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312888P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318749P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
PA (CURA-) CURAGEN CORP.
XX
XX TChernav VT, Spytek KA, Zernhusen BD, Paturajan M, Shinkets RA,
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE,
PI Gerlach VV, Taupier RV, Gusev VV, Colman SD, Wolanc AR, Pana CEA,
PI Furtak K, Grose WM, Alsobrook JP, Lepley DK, Rieger DK, Burgess CE,
XX
XX MPI: 2002-706998/76.
DR N-PSDB; AD116603.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
XX Claim 1; SEQ ID NO 140; 1496pp; English.
XX
CC This invention relates to a novel nucleic acids, and encoded polypeptides
CC thereof, which have properties related to the stimulation of biochemical
CC or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for
CC diagnostic and prognostic assays and furthermore in the treatment of
CC diverse pathological conditions. The present invention describes novel
CC human and murine NOVX proteins, as well as methods to modulate their
CC expression using antisense oligos, ribozymes and peptide nucleic acids.
CC The NOVX polypeptides, polynucleotides and antibodies are useful in
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC treating or preventing diseases such as inflammation, autoimmune
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis,
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC and epilepsy. Accordingly, these molecules have many activities including
CC cyostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC antisthmatic, nephrotoxic, antiarthritic, hepatocytic,
CC neuroprotective, neurotropic, antibacterial, virocidic, antiparasitic,
CC relaxant and anticonvulsant. In addition, they are useful in screening
CC assays to identify small molecules that modulate or inhibit, for example,
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC used as in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. This polypeptide is a human NOVX protein of the
CC invention.
XX
XX Sequence 781 AA;
XX
XX
XX Query Match 100.0%; Score 82; DB 5; Length 781;
Best, Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VGTSVIQVTAHDADDP 16
Db 165 VGTSVIQVTAHDADDP 180
AD116606
ID AD116606 standard; protein; 781 AA.
XX
AC AD116606;
XX
XX 15-APR-2004 (first entry)
XX
XX Human NOVX protein to treat human pathological conditions SeqID142.
DE
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
XX inflammation; autoimmune disorder; allergy; blood disorder;
XX acquired immunodeficiency syndrome; AIDS; obesity; ascema;
XX immunoglobulin (Ig) A nephropathy; cirrhosis; arthritis;
XX Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
XX cytostatic; cardiant; antiinflammatory; immunosuppressive; antiallergic;
XX haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
XX antisthmatic; nephrotoxic; antiarthritic; hepatocytic;
XX neuroprotective; neurotropic; antibacterial; virocidic; antiparasitic;
XX relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
XX chromosome mapping; tissue typing; pharmacogenomic.
XX
XX Homo sapiens.
OS
XX
XX WC200268649-A2.
XX
XX PD 06-SEP-2002.

BS	Claim 1, SEQ ID NO 142; 1498pp; English.
XX	This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.
CC	Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of
CC	diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their
CC	expression using antisense oligos, ribozymes and peptide nucleic acids.
CC	The NOVX polypeptides, polynucleotides and antibodies are useful in
CC	treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
CC	atherosclerosis, cancer and diabetes. Furthermore, they may be used in
CC	treating or preventing diseases such as inflammation, autoimmune
CC	disorders, allergies, blood disorders, acquired immunodeficiency syndrome
CC	(AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
CC	arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
CC	and epilepsy. Accordingly, these molecules have many activities including
CC	cytostatic, cardiant, anti-inflammatory, immunosuppressive, antiallergic,
CC	haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
CC	antianasthmatic, nephroprotective, antiarthritic, hepatotropic,
CC	neuroprotective, neurotropic, antibacterial, vitruide, antiparasitic,
CC	relaxant and anticonvulsant. In addition, they are useful in screening
CC	assays to identify small molecules that modulate or inhibit, for example,
CC	neurogenesis, wound healing and angiogenesis. The nucleic acids are also
CC	used as in chromosome mapping, tissue typing, preventive medicine and
CC	pharmacogenomics. This polypeptide is a human NOVX protein of the
CC	invention.
XX	
SO	Sequence 781 AA:
	Query Match 100.0%; Score 82; DB 5; Length 781;
	Best Local Similarity 100.0%; Pred. No. 5,1e-06;
	Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	165 VGTSVYQVTAAHDADDP 180
	RESULT 12
ID	ABR40114
XX	ABR40114 standard; protein; 781 AA.
XX	
AC	ABR40114;
XX	
DT	04-JUL-2003 (first entry)
XX	
DE	Human cell adhesion and extracellular matrix protein, CADSCM-11.
XX	
KM	Human; anti-HIV; antiallergic; cerebroprotective; antiParkinsonian;
KM	anticonvulsant; neurotropic; neuroprotective; immunosuppressive;
KM	dermatological; anti-inflammatory; cytostatic; antiarteriosclerotic;
KM	Gene therapy; cell adhesion; extracellular matrix; CADSCM;
KM	immune system disorder; AIDS; allergy; neurological disorder; stroke;
KM	Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
KM	Parkinson palsy; connective tissue disorder; systemic lupus erythematosus;
KM	genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
KM	atherosclerosis.
XX	
OS	Homo sapiens.
XX	
XX	W02003027230-A2.
EN	
PD	
XX	03-APR-2003.
XX	
XX	02-AUG-2002; 2002WO-US024649.
PF	
XX	
ER	03-AUG-2001; 2001US-0309964P.
ER	17-AUG-2001; 2001US-0310119P.
ER	31-AUG-2001; 2001US-0310791P.
ER	07-SEP-2001; 2001US-0317896P.

21-SEP-2001; 2001US-0324781P.
 05-OCT-2001; 2001US-0327606P.
 PR 12-OCT-2001; 2001US-0328960P.
 PR 09-NOV-2001; 2001US-0344471P.
 PR 17-MAY-2002; 2002US-0361291P.
 XX
 PA (INCYTE GENOMICS INC.)
 XX
 PI Buford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
 PI Forsythe TJ, Elliott VS, Griffin JA, Gorvad AE, Azimzai Y;
 PI Kallik DA, Xu Y, Honchell CD, Baughn MR, Gierzen KT, Lee S;
 PI Walla NK, Tang YT, Nguyen DB, Becha SD, Lee ST, Ramkumar J;
 XX
 DR WPI; 2003-354645/33.
 DR N-PSDB; ACC00402.
 XX
 PT New human cell adhesion and extracellular matrix proteins (CADECM),
 PT useful for diagnosing, treating or preventing disorders associated with
 PT aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
 PT or stroke.
 XX
 PS Claim 1; Page 192-194; 234pp; English.
 XX
 CC The present invention relates to novel human cell adhesion and
 CC extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
 CC sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
 CC and proteins are useful in diagnosing, treating and preventing disorders
 CC associated with aberrant expression of CADECM, such as immune system
 CC disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
 CC Parkinson's disease or epilepsy), developmental disorders (e.g. Down's
 CC syndrome or cerebral palsy), connective tissue disorders (e.g. systemic
 CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
 CC proliferative disorders (e.g. cancer or atherosclerosis)
 CC
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 82; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGTSVIQVTADDDP 16
 DB 165 VGTSVIQVTADDDP 180
 RESULT 13
 ID ADA01366 standard; protein; 781 AA.
 XX
 AC ADA01366;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human PRO polypeptide #49.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
 KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
 KW microvascular endothelial cell; endothelial cell tube formation;
 KW sports-related joint problem; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; osteopathic; antineumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN US2003068779-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245107.
 XX
 PR 09-MAY-2001; 2001US-0290589P.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.

XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;
 XX
 DR WPI; 2003-625484/59.
 DR N-PSDB; ADA01365.
 XX
 PT Novel isolated PRO1313, PRO20080 or PRO21393 polypeptide useful for
 PT stimulating proliferation of human microvascular endothelial cells, and
 PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 PT cells.
 XX
 PS Claim 11; Fig 98; 307pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for inducing endothelial cell
 CC tube formation and for treating sports-related joint problems, articular
 CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 CC represents a human PRO polypeptide of the invention.
 CC
 SQ Sequence 781 AA;
 Query Match 100.0%; Score 82; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VGTSVIQVTADDDP 16
 DB 165 VGTSVIQVTADDDP 180
 RESULT 14
 ID ADA43795 standard; protein; 781 AA.
 XX
 AC ADA43795;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted/transmembrane polypeptide PRO34009.
 XX
 KW Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2003064474-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US0270399.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX MPI: 2003-605867/57.
DR N-PSDB; ADA43562.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 11; Fig 98; 308pp; English.
XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6108, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 82; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5,1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VGTSVIGVTADADDP 16
Db 165 VGTSVIGVTADADDP 180
XX
XX RESULT 15
ADA43563
ID ADA43563 standard; protein; 781 AA.
XX
XX ADA43563;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human secreted/transmembrane polypeptide PRO34009.
DS
XX

XX Human; PRO; secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cytostatic; vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2003073196-A1.
PN
XX
XX 17-APR-2003.
PD
XX
XX 18-SEP-2002; 2002US-00246210.
PF
XX
XX 04-APR-2001; 2001US-0282199P.
PR 29-AUG-2001; 2001WO-US0270399.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GENTH) GENENTECH INC.
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX MPI: 2003-743814/70.
DR N-PSDB; ADA43562.
XX
XX New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT PRO21383 useful for stimulating the proliferation or differentiation of
PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
XX Claim 11; Fig 98; 307pp; English.
XX
XX The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6108, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence represents a PRO protein.
XX
XX Sequence 781 AA;
SQ
Query Match 100.0%; Score 82; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5,1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VGTSVIGVTADADDP 16

Wed Dec 8 11:46:25 2004

us-09-788-051-14.rag

Page 11

Db 165 VGTSVIQTADADDP 180

Search completed: December 8, 2004, 10:13:06
Job time : 6.62102 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 / Search time 16.3495 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-14

Perfect score: 82

Sequence: 1 VGTSVIQVTAHDADP 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pdp:*
- 2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pdp:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdp:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdp:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pdp:*
- 6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pdp:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pdp:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pdp:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pdp:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	82	100.0	16 10 US-09-788-051-14	Sequence 14, Appl
2	82	100.0	48 10 US-09-788-051-8	Sequence 8, Appl
3	82	100.0	493 15 US-10-072-012-482	Sequence 482, Appl
4	82	100.0	607 15 US-10-258-951-74	Sequence 74, Appl
5	82	100.0	620 10 US-09-788-051-7	Sequence 7, Appl
6	82	100.0	636 10 US-09-788-051-4	Sequence 4, Appl
7	82	100.0	781 9 US-09-860-858-2	Sequence 2, Appl
8	82	100.0	781 14 US-10-245-752-98	Sequence 98, Appl
9	82	100.0	781 14 US-10-245-859-98	Sequence 98, Appl
10	82	100.0	781 14 US-10-245-103-98	Sequence 98, Appl
11	82	100.0	781 14 US-10-245-107-98	Sequence 98, Appl
12	82	100.0	781 14 US-10-245-143-98	Sequence 98, Appl
13	82	100.0	781 14 US-10-245-771-98	Sequence 98, Appl

14	82	100.0	781 14 US-10-245-851-98	Sequence 98, Appl
15	82	100.0	781 14 US-10-245-863-98	Sequence 98, Appl
16	82	100.0	781 14 US-10-237-535-98	Sequence 98, Appl
17	82	100.0	781 14 US-10-238-183-98	Sequence 98, Appl
18	82	100.0	781 14 US-10-238-283-98	Sequence 98, Appl
19	82	100.0	781 14 US-10-238-370-98	Sequence 98, Appl
20	82	100.0	781 14 US-10-245-055-98	Sequence 98, Appl
21	82	100.0	781 14 US-10-245-147-98	Sequence 98, Appl
22	82	100.0	781 14 US-10-245-730-98	Sequence 98, Appl
23	82	100.0	781 14 US-10-245-739-98	Sequence 98, Appl
24	82	100.0	781 14 US-10-246-210-98	Sequence 98, Appl
25	82	100.0	781 14 US-10-239-156-98	Sequence 98, Appl
26	82	100.0	781 14 US-10-243-024-98	Sequence 98, Appl
27	82	100.0	781 14 US-10-243-409-98	Sequence 98, Appl
28	82	100.0	781 14 US-10-245-621-98	Sequence 98, Appl
29	82	100.0	781 14 US-10-245-880-98	Sequence 98, Appl
30	82	100.0	781 14 US-10-245-033-98	Sequence 98, Appl
31	82	100.0	781 14 US-10-243-035-98	Sequence 98, Appl
32	82	100.0	781 14 US-10-245-185-98	Sequence 98, Appl
33	82	100.0	781 14 US-10-245-427-98	Sequence 98, Appl
34	82	100.0	781 14 US-10-245-473-98	Sequence 98, Appl
35	82	100.0	781 14 US-10-245-770-98	Sequence 98, Appl
36	82	100.0	781 14 US-10-245-877-98	Sequence 98, Appl
37	82	100.0	781 14 US-10-245-976-98	Sequence 98, Appl
38	82	100.0	781 14 US-10-243-320-98	Sequence 98, Appl
39	82	100.0	781 14 US-10-162-435-13	Sequence 13, Appl
40	82	100.0	781 14 US-10-242-743-98	Sequence 98, Appl
41	82	100.0	781 14 US-10-242-845-98	Sequence 98, Appl
42	82	100.0	781 14 US-10-237-636-98	Sequence 98, Appl
43	82	100.0	781 14 US-10-238-325-98	Sequence 98, Appl
44	82	100.0	781 14 US-10-238-346-98	Sequence 98, Appl
45	82	100.0	781 14 US-10-238-411-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-14
Sequence 14, Application US/09788051
Publicatation No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanag, Radote T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES A
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-14
Query Match 100.0%; Score 82; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VGTSVIQVTAHDADP 16
|||||

Db 1 VGTSVIQVTAHDADDP 16

RESULT 2

US-09-788-051-8

Sequence 8, Application US/0988051

Publication No. US2003014491A1

GENERAL INFORMATION:

APPLICANT: Godbole, Shubhada D

APPLICANT: Kuo, Chiaoyn

APPLICANT: Arterburn, Matthew C

APPLICANT: Yeung, George

APPLICANT: Palencia, Servando

APPLICANT: Tang, Y. Tom

APPLICANT: Lin, Chenghua

APPLICANT: Dimaec, Radcoje T

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND

FILE REFERENCE: HVS-39

CURRENT APPLICATION NUMBER: US/09/788,051

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 48

TYPE: PRT

ORGANISM: Homo sapiens

US-09-788-051-8

Query Match 100.0%; Score 82; DB 10; Length 48;

Best Local Similarity 100.0%; Pred. No. 6.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTAHDADDP 16

Db 33 VGTSVIQVTAHDADDP 48

RESULT 3

US-10-072-012-482

Sequence 482, Application US/10072012

Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchernev, Velizar

APPLICANT: Spytek, Kimberly

APPLICANT: Zernhusen, Bryan

APPLICANT: Paturajan, Meera

APPLICANT: Shmukev, Richard

APPLICANT: Li, Li

APPLICANT: Gangolli, Esha

APPLICANT: Padigaru, Murajidhara

APPLICANT: Anderson, David W.

APPLICANT: Raetelli, Luca

APPLICANT: Miller, Charles E.

APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Colman, Steven D.

APPLICANT: Wolenc, Adam R.

APPLICANT: Pena, Carol E. A

APPLICANT: Futak, Katarzyna

APPLICANT: Grosse, William M.

APPLICANT: Alsbrook II, John P.

APPLICANT: Lepley, Denise M.

APPLICANT: Rieser, Daniel K.

APPLICANT: Burgees, Catherine E.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-258

CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,412

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395

PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/266,406

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/266,767

PRIOR FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: 60/267,057

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/266,975

PRIOR FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: 60/267,459

PRIOR FILING DATE: 2001-02-08

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 482

LENGTH: 493

TYPE: PRT

ORGANISM: Homo sapiens

US-10-072-012-482

Query Match 100.0%; Score 82; DB 15; Length 493;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTAHDADDP 16

Db 165 VGTSVIQVTAHDADDP 180

RESULT 4

US-10-258-951-74

Sequence 74, Application US/10258951

Publication No. US20040033504A1

GENERAL INFORMATION:

APPLICANT: Agarwal, Pankaj

APPLICANT: Murdoch, Paul R.

APPLICANT: Rizvi, Safia K.

APPLICANT: Smith, Randall F.

APPLICANT: Xiang, Zhaoying

APPLICANT: Kabnick, Karen

APPLICANT: Lai, Ying-Ta

APPLICANT: Xie, Qing

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GPS0025

CURRENT APPLICATION NUMBER: US/10/258,951

CURRENT FILING DATE: 2002-10-28

PRIOR APPLICATION NUMBER: PCT/US01/13360

PRIOR FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: 60/199,963

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/203,336

PRIOR FILING DATE: 2000-05-11

PRIOR APPLICATION NUMBER: 60/207,087

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/207,546

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 74

LENGTH: 607

TYPE: PRT

ORGANISM: Homo sapiens

US-10-258-951-74

Query Match 100.0%; Score 82; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADHADDP 16
Db 165 VGTSVIQVTADHADDP 180

RESULT 5

US-09-788-051-7
Sequence 7, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: POLYNUCLEOTIDES
FILE REFERENCE: HVS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 620
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 82; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADHADDP 16
Db 149 VGTSVIQVTADHADDP 164

RESULT 6

US-09-788-051-4
Sequence 4, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiaoyun
APPLICANT: Atterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Dmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AND
FILE REFERENCE: POLYNUCLEOTIDES
FILE REFERENCE: HVS-39
CURRENT APPLICATION NUMBER: US/09/788,051
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0

SEQ ID NO 4
LENGTH: 636
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 82; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADHADDP 16
Db 165 VGTSVIQVTADHADDP 180

RESULT 7

US-09-860-868-2
Sequence 2, Application US/09860868
Patent No. US2002007657A1
GENERAL INFORMATION:
APPLICANT: Curtis, Roy A.J.
TITLE OF INVENTION: MEMBER AND USES THEREOF
FILE REFERENCE: 10448-050001
CURRENT APPLICATION NUMBER: US/09/860,868
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 60/205,674
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 781
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-860-868-2

Query Match 100.0%; Score 82; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGTSVIQVTADHADDP 16
Db 165 VGTSVIQVTADHADDP 180

RESULT 8

US-10-245-752-98
Sequence 98, Application US/10245752
Publication No. US20030064473A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C66
CURRENT APPLICATION NUMBER: US/10/245,752
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24

Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-245-859-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 VGTSVIQTADADDP 180

US-10-245-752-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 VGTSVIQTADADDP 180

US-10-245-859-98

Sequence 98, Application US/10245859
Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C78
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-245-103-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 VGTSVIQTADADDP 180

US-10-245-103-98

Sequence 98, Application US/10245103
Publication No. US20030068778A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C112
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-245-859-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 VGTSVIQTADADDP 180

US-10-245-103-98

Sequence 98, Application US/10245103
Publication No. US20030068778A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C112
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-245-103-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 165 VGTSVIQTADADDP 180

US-10-245-103-98

Sequence 98, Application US/10245103
Publication No. US20030068778A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe
APPLICANT: Watande, Colin
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3630R1C112
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25

Db 165 VGTSVIQVTAHDADDP 180

RESULT 11

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US-10-245-107-98
; Sequence 98, Application US/10245107
; Publication No. US20030068795A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Matande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C91
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98

Query Match 100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Cy 1 VGTSVIQVTAHDADDP 16

Db 165 VGTSVIQVTAHDADDP 180

RESULT 12

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US-10-245-143-98
; Sequence 98, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin
```

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Matande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C90

CURRENT APPLICATION NUMBER: US/10/245,143

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/065027

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/079689

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/090557

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116

SEQ ID NO 98

LENGTH: 781

TYPE: PRT

ORGANISM: Homo Sapien

US-10-245-143-98

Query Match 100.0%; Score 82; DB 14; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 VGTSVIQVTAHDADDP 16

Db 165 VGTSVIQVTAHDADDP 180

US-10-245-771-98

Sequence 98, Application US/10245771

Publication No. US20030068781A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton, Dan

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Guiney, Austin

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe

APPLICANT: Matande, Colin

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Fong, Sherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3630R1C98

CURRENT APPLICATION NUMBER: US/10/245,771

CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/059114

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-98
```

```

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 VGTSVIQVTAHADDP 16
Db      165 VGTSVIQVTAHADDP 180
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RESULT 14
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Warabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245, 851
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98
```

```

Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 VGTSVIQVTAHADDP 16
Db      165 VGTSVIQVTAHADDP 180
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RESULT 15
US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Warabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C70
; CURRENT APPLICATION NUMBER: US/10/245, 883
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98
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Query Match      100.0%; Score 82; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Wed Dec 8 11:46:26 2004

us-09-788-051-14.rapb

Page 7

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| | | | | | | | | |
Db 165 VGTSVICVTAHADDP 180

Search completed: December 8, 2004, 11:34:30
Job time : 16.3495 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 1.90791 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-14
Perfect score: 82
Sequence: 1 VGTSVIQVTAHDADDP 16

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	89.0	109	3	US-09-187-859-5
2	73	89.0	109	4	US-09-839-542B-5
3	73	89.0	109	4	US-09-535-852-5
4	73	89.0	615	2	US-08-738-349-12
5	73	89.0	693	2	US-08-738-349-6
6	73	89.0	693	4	US-09-919-497-55
7	73	89.0	796	1	US-08-188-228-58
8	73	89.0	796	1	US-08-332-643-52
9	73	89.0	796	1	US-08-332-638-58
10	73	89.0	796	2	US-08-738-349-2
11	73	89.0	796	2	US-08-738-349-4
12	73	89.0	796	4	US-09-654-328-2
13	73	89.0	109	3	US-09-187-859-11
14	73	89.0	109	4	US-09-839-542B-11
15	73	89.0	109	4	US-09-535-852-11
16	73	89.0	653	1	US-08-188-228-46
17	73	89.0	653	1	US-08-332-638-46
18	73	89.0	109	3	US-09-187-859-17
19	73	89.0	109	4	US-09-839-542B-17
20	73	89.0	109	4	US-09-535-852-17
21	73	89.0	780	1	US-08-188-228-50
22	73	89.0	780	1	US-08-332-643-44
23	73	89.0	780	1	US-08-332-638-50
24	73	89.0	109	3	US-09-187-859-8
25	73	89.0	109	4	US-09-839-542B-8
26	73	89.0	109	4	US-09-535-852-8
27	73	89.0	109	3	US-09-187-859-23

28	60	73.2	109	4	US-09-839-542B-23	Sequence 23, Appl
29	60	73.2	109	4	US-09-535-852-23	Sequence 23, Appl
30	59	72.0	532	1	US-08-188-228-44	Sequence 44, Appl
31	59	72.0	532	1	US-08-332-638-44	Sequence 44, Appl
32	59	72.0	793	1	US-08-188-228-54	Sequence 54, Appl
33	59	72.0	793	1	US-08-332-643-48	Sequence 48, Appl
34	59	72.0	793	1	US-08-332-638-54	Sequence 54, Appl
35	59	72.0	799	1	US-08-188-228-42	Sequence 42, Appl
36	59	72.0	799	1	US-08-332-638-42	Sequence 42, Appl
37	56	68.3	712	2	US-08-474-067-2	Sequence 2, Appl
38	56	68.3	712	2	US-08-474-067-5	Sequence 5, Appl
39	56	68.3	712	2	US-08-474-068A-2	Sequence 2, Appl
40	56	68.3	712	2	US-08-474-068A-5	Sequence 5, Appl
41	56	68.3	712	2	US-08-472-481-2	Sequence 2, Appl
42	56	68.3	713	1	US-08-188-228-62	Sequence 62, Appl
43	56	68.3	713	1	US-08-332-643-56	Sequence 56, Appl
44	56	68.3	713	1	US-08-332-638-62	Sequence 62, Appl
45	56	68.3	717	2	US-08-474-067-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-187-859-5
; Sequence 5, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086, 407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-187-859-5

Query Match      89.0%; Score 73; DB 3; Length 109;
Best Local Similarity 93.8%; Pred. No. 6,4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 VGTSVIQVTAHDADDP 16
| | | | | | | | | | | | | | | |
DB      15 VGTSVIQVTAHDADDP 30

RESULT 2
US-09-839-542B-5
; Sequence 5, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REFERENCE: 100086, 407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-542B-5
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Query Match 89.0%; Score 73; DB 4; Length 109;
Best Local Similarity 93.8%; Pred. No. 6,4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIQTVAHDADDP 16
Db 15 VGTSVIQTVAHDADDP 30

RESULT 3

US-09-535-852-5
Sequence 5, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-535-852-5

Query Match 89.0%; Score 73; DB 4; Length 109;
Best Local Similarity 93.8%; Pred. No. 6,4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIQTVAHDADDP 16
Db 15 VGTSVIQTVAHDADDP 30

RESULT 4

US-08-728-349-12
Sequence 12, Application US/08728349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-738-349-12

Query Match 89.0%; Score 73; DB 2; Length 615;
Best Local Similarity 93.8%; Pred. No. 5,4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VGTSVIQTVAHDADDP 16
Db 167 VGTSVIQTVAHDADDP 182

RESULT 5

US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-738-349-6

Query Match 89.0%; Score 73; DB 2; Length 693;
Best Local Similarity 93.8%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
DB 174 VGTSVIQVTASDADDP 189

RESULT 6

US-09-919-497-55
Sequence 55, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SEQ ID NO 55
LENGTH: 693
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 89.0%; Score 73; DB 4; Length 693;
Best Local Similarity 93.8%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
DB 174 VGTSVIQVTASDADDP 189

RESULT 7

US-08-188-228-58
Sequence 58, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 89.0%; Score 73; DB 1; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16
DB 174 VGTSVIQVTASDADDP 189

RESULT 8

US-08-332-643-52
Sequence 52, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query Match 89.0%; Score 73; DB 1; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQVTADDDP 16

Db 174 VGTSVIQTASDADDP 189

RESULT 9

US-08-332-638-58

Sequence 58, Application US/08332638
Patent No. 5646250

GENERAL INFORMATION:

APPLICANT: Suzuki, Shintaro

TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESS: Boston

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638

FILING DATE: 01-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643

FILING DATE: 17 APR 1992

APPLICATION NUMBER: US/08/049,460

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5646250and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31340

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-332-638-58

Query Match 89.0%; Score 73; DB 1; Length 796;

Best Local Similarity 93.8%; Pred. No. 7.4e-05;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQTASDADDP 16

Db 174 VGTSVIQTASDADDP 189

RESULT 10

US-08-738-349-2

Sequence 2, Application US/08738349
Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Amann, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349

FILING DATE: 25-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/364,439

FILING DATE:

APPLICATION NUMBER: US 08/112,061

FILING DATE: 26-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Barker, M. P.

REGISTRATION NUMBER: 32,013

REFERENCE/DOCKET NUMBER: 02481.1323-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 796 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-738-349-2

Query Match 89.0%; Score 73; DB 2; Length 796;

Best Local Similarity 93.8%; Pred. No. 7.4e-05;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGTSVIQTASDADDP 16

Db 174 VGTSVIQTASDADDP 189

RESULT 11

US-08-738-349-4

Sequence 4, Application US/08738349
Patent No. 5869638

GENERAL INFORMATION:

APPLICANT: Takeshita, Sunao

APPLICANT: Okazaki, Makoto

APPLICANT: Kawai, Shinji

APPLICANT: Tsujimura, Atsushi

APPLICANT: Amann, Egon

TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,349


```
; FILING DATE: 25-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/364,439
; FILING DATE:
; APPLICATION NUMBER: US 08/112,061
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. P.
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 02481.1323-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 796 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-738-349-4
```

```
Query Match      89.0%; Score 73; DB 2; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VGTSVIQVTADDDP 16
Db      174 VGTSVIQVTADDDP 189
```

```
RESULT 12
US-09-654-328-2
; Sequence 2, Application US/09654328
; Patent No. 6787136
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael B.
; APPLICANT: Valencia, Xavier
; TITLE OF INVENTION: Methods and Compositions for Treatment
; TITLE OF INVENTION: of Inflammatory Disease Using Cadherin-11 Modulating Agents
; FILE REFERENCE: B0801/7187/ERP/MAT
; CURRENT APPLICATION NUMBER: US/09/654,328
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/153,456
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: US 60/153,490
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2:
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-654-328-2
```

```
Query Match      89.0%; Score 73; DB 4; Length 796;
Best Local Similarity 93.8%; Pred. No. 7.4e-05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VGTSVIQVTADDDP 16
Db      174 VGTSVIQVTADDDP 189
```

```
RESULT 13
US-09-187-859-11
; Sequence 11, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
```

```
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-187-859-11
```

```
Query Match      86.6%; Score 71; DB 3; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VGTSVIQVTADDDP 16
Db      15 VGTSVIQVTADDDP 30
```

```
RESULT 14
US-09-839-542B-11
; Sequence 11, Application US/09839542B
; Patent No. 6568996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-839-542B-11
```

```
Query Match      86.6%; Score 71; DB 4; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VGTSVIQVTADDDP 16
Db      15 VGTSVIQVTADDDP 30
```

```
RESULT 15
US-09-535-852-11
; Sequence 11, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-535-852-11
```

```
Query Match      86.6%; Score 71; DB 4; Length 109;
Best Local Similarity 87.5%; Pred. No. 1.5e-05;
```

Wed Dec 8 11:46:25 2004

us-09-788-051-14.ra1

Page 6

Matches	14;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	VGSTVIGVTAHADADP	16						
		:							
Db	15	VGSTVIGVTAHADADP	30						

```
Search completed: December 8, 2004, 10:01:14
Job time : 1.90791 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13, Search time 15.6086 Seconds
(without alignments)
1189.717 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVPSVETAGPCTLVGRL.....APDREARAHNLTVALTEL 193

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	537	54.2	796	2 A38992	cadherin 11 precurs
2	532	53.7	796	2 I49556	cadherin-11 - mus
3	532	53.7	796	2 A53584	OB-cadherin precurs
4	529	53.4	796	2 I48277	cadherin-11 - mus
5	521	52.6	793	2 D38992	cadherin 8 - human
6	485	49.0	789	2 I52701	K-cadherin - rat
7	484	48.9	790	2 I37016	cadherin-6 - human
8	460	46.5	790	2 I50178	cadherin-6B - chick
9	448	45.3	785	2 I50180	cadherin-7 - chick
10	421	42.5	790	2 G02678	cadherin-14 - huma
11	421	42.5	790	2 I51638	F-cadherin - Afric
12	411	41.5	794	2 I59372	cadherin 12 - huma
13	314.5	31.8	784	1 I0HUC5	cadherin 5 precurs
14	229.5	23.2	5147	1 I0FFTM	cadherin-related t
15	218	22.0	814	2 G02878	cadherin-15 precu
16	215	21.7	2809	2 G30213	G-cadherin - sea u
17	212.5	21.5	3034	2 T14119	M-cadherin - sea u
18	210	21.2	730	1 I0MSCM	seven-pass transme
19	205	20.7	906	1 I0XLC2	N-cadherin - mouse
20	203	20.5	712	1 I0MSTC	N-cadherin 2 precu
21	203	20.5	717	1 I0MSTC	T-cadherin precurs
22	202	20.4	905	1 I0XLC1	N-cadherin 2 - chi
23	200	20.2	887	1 I0XLC1	N-cadherin 1 precu
24	198.5	20.1	491	1 I0BOCP	P-cadherin - bovin
25	198.5	20.1	713	2 B38992	cadherin 13 precu
26	196	19.8	4351	2 T00252	MEGFL protein - ra
27	191	19.3	906	1 I0MSCN	N-cadherin precurs
28	190.5	19.2	827	1 A53954	L1-cadherin precu
29	189.5	19.1	889	2 T09055	protocadherin 68 -

30	188	19.0	906	1 I0HUCN	cadherin 2 precurs
31	186.5	18.8	826	2 B55363	desmocollin, type
32	186.5	18.8	832	2 S55396	LI-cadherin - huma
33	186.5	18.8	896	2 A55363	desmocollin, type
34	186	18.8	916	2 C38992	cadherin 4 precurs
35	185.5	18.7	701	2 T17243	hypothetical prote
36	185.5	18.7	912	1 I0CHCN	N-cadherin precurs
37	185.5	18.7	4307	2 T20721	hypothetical prote
38	184	18.6	829	1 I0HUCP	cadherin 3 precurs
39	183.5	18.5	822	1 I0MSCP	P-cadherin precurs
40	183	18.5	877	1 I0BOCN	N-cadherin precurs
41	182	18.4	913	1 A47543	R-cadherin precurs
42	181.5	18.3	896	2 I45858	desmocollin - bovi
43	178	18.0	913	1 I0CHCR	R-cadherin precurs
44	175.5	17.7	294	2 A54742	desmocollin 3 - mo
45	175.5	17.7	732	1 I0CHCB	B-cadherin precurs

ALIGNMENTS

RESULT 1

A38992
cadherin 11 precursor - human
N:Alternate names: OB-cadherin, osteoblast
C:Species: Homo sapiens (man)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Jul-2004
C:Accession: A38992
R:SuZuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A:Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous
A:Reference number: S24305; PMID:91283540; PMID:2059658
A:Accession: A38992
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-796 <SUZ>
A:Cross-references: UNIPROT: P55287; GB: I34056; NID: G506403; PIRN: AAA35622.1; PID: G50640
C:Gene(s):
A:Gene: GDB: CDH11; OB
A:Cross-references: GDB: 512891; OMIM: 600023
A:Map position: 16c22.1-16c22.1
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication
F:56-159/Domain: cadherin repeat homology <CR1>
F:162-268/Domain: cadherin repeat homology <CR2>
F:271-383/Domain: cadherin repeat homology <CR3>
F:386-488/Domain: cadherin repeat homology <CR4>

Query Match 54.2%; Score 537; DB 2; Length 796;
Best Local Similarity 51.6%; Pred. No. 2.6e-39;

Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY	2	LYQFSVETAGPCTLVGRADPDLDGNALNAYSLIDEGEGEAFSISTDLGRDGLTV 61	
DB	272	LYQMSVSEAAVPGEBGRVAKDPDLDGNGLVYTNIVDSGMESEBITTDYTGQGVTL 331	
QY	62	RKPLDPESQSYSFREYVATNTLIDPAYLRGPFKQVAVQDAPEPPATQAAVHT 121	
DB	332	KKVDDETERAVSLKKEAANVHIDPKFTNGPFKTVYKISVEDADEPMLAASYIHE 391	
QY	122	VPEKNKAGTLVQGISADDSFASPIRYSILPHSDPERCFISQPEGTHTAFLDREAR 181	
DB	392	VQENMAAGTVAGRVAKDPAANSPIRYSIDNHTDLDREFTINPEDEGFIKTKPDRREBT 451	
QY	182	AMNLTVALTEL 193	
DB	452	AMNLTVAABI 463	
RESULT 2			
I49556		cadherin-11 - mouse	
C:Species: Mus musculus (house mouse)			

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I49556
 R:Kimura, Y.; Matsunami, H.; Inoue, T.; Shimamura, K.; Uchida, N.; Ueno, T.; Miyazaki, T.
 Dev. Biol. 169, 347-358, 1995
 A>Title: Cadherin-11 expressed in association with mesenchymal morphogenesis in the head
 A/Reference number: 149556; MUID:95269887; PMID:7750650
 A/Accession: I49556
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; GB:D31963; NID:974190; PIDN:BA06730.1; PID:974191
 C/Superfamily: cadherin; cadherin repeat homology
 F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 53.7%; Score 532; DB 2; Length 796;
 Best Local Similarity 50.8%; Pred. No. 7.1e-39; Indels 0; Gaps 0;
 Matches 98; Conservative 42; Mismatches 53;

QY 1 SLVQSVYETAGPGLVGRRLAOPDPLGDNALMAVSLIDEGSEAFSISTDLQGRDGLT 60
 DB 271 SVYQMSVSEAAVPGEEVGRVAKDPDGENGLVTYINVDGDELFEITTDVETQGVVK 330
 QY 61 VRKPLDESOQRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQADPEPPAQAAYHL 120
 DB 331 LKRPVDEFTKRAYSLKLEAAVNHIDPKFISNGPKDVTWKISVEDADEPMPFLAPSYIH 390
 QY 121 TVPENKAPGTLVQGISADLDSPPASPRYSILPHSDPERCFISIOPEEGTHTAPADREA 180
 DB 391 EVQENAAAGTVGVGHAKDPDANSPRYSIDRHTDLDREFTINPEDGFIKTKPLDREE 450
 QY 181 RAMNLTIVLATEL 193
 DB 451 TAWNLISVFAADI 463

RESULT 3

OB-cadherin precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C/Accession: A53584
 R:Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.; Kudo, A.; Mann, E.
 J. Biol. Chem. 269, 12092-12098, 1994
 A>Title: Molecular cloning and characterization of OB-cadherin, a new member of cadherin
 A/Reference number: A53584; MUID:94216322; PMID:8163513
 A/Accession: A53584
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-796 <OKA>
 A/Cross-references: UNIPROT:P55288; GB:D31253; NID:994774; PIDN:BA04797.1; PID:9594775
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: transmembrane protein
 F:156-159/Domain: cadherin repeat homology <CR1>
 F:162-268/Domain: cadherin repeat homology <CR2>
 F:386-488/Domain: cadherin repeat homology <CR4>

Query Match 53.7%; Score 532; DB 2; Length 796;
 Best Local Similarity 50.8%; Pred. No. 7.1e-39; Indels 0; Gaps 0;
 Matches 98; Conservative 42; Mismatches 53;

QY 1 SLVQSVYETAGPGLVGRRLAOPDPLGDNALMAVSLIDEGSEAFSISTDLQGRDGLT 60
 DB 271 SVYQMSVSEAAVPGEEVGRVAKDPDGENGLVTYINVDGDELFEITTDVETQGVVK 330
 QY 61 VRKPLDESOQRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQADPEPPAQAAYHL 120
 DB 331 LKRPVDEFTKRAYSLKLEAAVNHIDPKFISNGPKDVTWKISVEDADEPMPFLAPSYIH 390
 QY 121 TVPENKAPGTLVQGISADLDSPPASPRYSILPHSDPERCFISIOPEEGTHTAPADREA 180
 DB 391 EVQENAAAGTVGVGHAKDPDANSPRYSIDRHTDLDREFTINPEDGFIKTKPLDREE 450
 QY 181 RAMNLTIVLATEL 193

DB 451 TAWNLISVFAADI 463

RESULT 4

cadherin-11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I48277
 R:Hoffmann, I.; Balling, R.
 Dev. Biol. 169, 337-346, 1995
 A>Title: Cloning and expression analysis of a novel mesodermally expressed cadherin.
 A/Reference number: I48277; MUID:95269886; PMID:7750649
 A/Accession: I48277
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-796 <RES>
 A/Cross-references: UNIPROT:P55288; EMBL:X77557; NID:9642796; PIDN:CA054674.1; PID:966666
 C/Superfamily: cadherin; cadherin repeat homology
 F:156-159/Domain: cadherin repeat homology <CDH>

Query Match 53.4%; Score 529; DB 2; Length 796;
 Best Local Similarity 50.3%; Pred. No. 1.3e-38; Indels 0; Gaps 0;
 Matches 97; Conservative 43; Mismatches 53;

QY 1 SLVQSVYETAGPGLVGRRLAOPDPLGDNALMAVSLIDEGSEAFSISTDLQGRDGLT 60
 DB 271 SVYQMSVSEAAVPGEEVGRVAKDPDGENGLVTYINVDGDELFEITTDVETQGVVK 330
 QY 61 VRKPLDESOQRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQADPEPPAQAAYHL 120
 DB 331 LKRPVDEFTKRAYSLKLEAAVNHIDPKFISNGPKDVTWKISVEDADEPMPFLAPSYIH 390
 QY 121 TVPENKAPGTLVQGISADLDSPPASPRYSILPHSDPERCFISIOPEEGTHTAPADREA 180
 DB 391 EVQENAAAGTVGVGHAKDPDANSPRYSIDRHTDLDREFTINPEDGFIKTKPLDREE 450
 QY 181 RAMNLTIVLATEL 193
 DB 451 TAWNLISVFAADI 463

RESULT 5

cadherin 8 - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
 C/Accession: D38992
 R:Suzuki, S.; Sano, K.; Tanihara, H.
 Cell Regul. 2, 261-270, 1991
 A>Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
 A/Reference number: D38992; MUID:91283540; PMID:2059658
 A/Accession: D38992
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-793 <SD>
 A/Cross-references: GB:I34060; NID:9506411; PIDN:AA33628.1; PID:9506412
 C/Genetics:
 A/Gene: GDB:CDH8
 A/Cross-references: GDB:5822911
 C/Superfamily: cadherin; cadherin repeat homology
 C/Keywords: calcium binding; cell adhesion; duplication
 F:163-269/Domain: cadherin repeat homology <CDH>

Query Match 52.6%; Score 521; DB 2; Length 793;
 Best Local Similarity 49.7%; Pred. No. 6.6e-38; Indels 0; Gaps 0;
 Matches 96; Conservative 41; Mismatches 56;

QY 1 SLVQSVYETAGPGLVGRRLAOPDPLGDNALMAVSLIDEGSEAFSISTDLQGRDGLT 60

Db 272 SLVHFSVPEDEVLTGTAIGRVKANKDQIGENAKSSYDIIDGDTALFEITSDAQADGIIR 331
 QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEETKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVSSTYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVHENAAINSVIGQVATADPDITSSPIRFSIDRHTDLERQFNINADDKITLATPLREL 451
 QY 181 RAMHNTLVATLTEL 193
 Db 452 SVMHNTIVATLTEL 464

RESULT 6
 K-cadherin - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I52701
 R/Xiang, Y.Y.; Tanaka, M.; Suzuki, M.; Igarashi, H.; Kiyokawa, E.; Naito, Y.; Ohtawara, Cancer Res. 54, 3034-3041, 1994
 A/Title: Isolation of complementary DNA encoding K-cadherin, a novel rat cadherin prefer A/Reference number: I52701; MUID:94243827; PMID:8187093
 A/Accession: I52701
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-789 <RES>
 A/Cross-references: UNIPROT:P55280; GB:D25290; NID:9435460; PIDN:BA04975.1; PID:9435461
 A/Gene: KCAD
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 49.0%; Score 485; DB 2; Length 789;
 Best Local Similarity 46.1%; Pred. No. 9.7e-35;
 Matches 89; Conservative 44; Mismatches 60; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGTLVGRRAQDPDLGNALMAYSLIDGSGSEAFSISTDLQGRGLLT 60
 Db 271 STYQFPTPESSPPGPPIGRIRKASDADVGEMAEIYSITDGGHDMFVITDQETQEGIIIT 330
 QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEETKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVSSTYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVHENAAINSVIGQVATADPDITSSPIRFSIDRHTDLERQFNINADDKITLATPLREL 451
 QY 181 RAMHNTLVATLTEL 193
 Db 452 SVMHNTIVATLTEL 464

RESULT 7
 137016
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 C/Accession: U137016
 R/Shimoyama, Y.; Gotch, M.; Terasaki, T.; Kitajima, M.; Hirohashi, S. Cancer Res. 55, 2206-2211, 1995
 A/Title: Isolation and sequence analysis of human cadherin-6 complementary DNA for the A/Reference number: U137016; MUID:95262134; PMID:7743525
 A/Accession: U137016
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <RES>
 A/Cross-references: UNIPROT:P55285; GB:D31784; NID:974184; PIDN:BA06562.1; PID:974185
 A/Gene: CDB:CDH6

A/Cross-references: GDB:5822508
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 48.9%; Score 484; DB 2; Length 790;
 Best Local Similarity 45.1%; Pred. No. 1.2e-34;
 Matches 87; Conservative 47; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGTLVGRRAQDPDLGNALMAYSLIDGSGSEAFSISTDLQGRGLLT 60
 Db 271 STYQFPTPESSPPGPPIGRIRKASDADVGEMAEIYSITDGGHDMFVITDQETQEGIIIT 330
 QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEETKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVSSTYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVHENAAINSVIGQVATADPDITSSPIRFSIDRHTDLERQFNINADDKITLATPLREL 451
 QY 181 RAMHNTLVATLTEL 193
 Db 452 SVMHNTIVATLTEL 464

RESULT 8
 150178
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: U150178
 R/Nakagawa, S.; Takeichi, M. Development 121, 1321-1332, 1995
 A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe A/Reference number: U150178; MUID:95309115; PMID:7540531
 A/Accession: U150178
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-790 <NAK>
 A/Cross-references: UNIPROT:Q90762; GB:D42149; NID:9867998; PIDN:BA07720.1; PID:986799
 C/Superfamily: cadherin; cadherin repeat homology
 F/162-268/Domain: cadherin repeat homology <CDH>

Query Match 46.5%; Score 460; DB 2; Length 790;
 Best Local Similarity 43.0%; Pred. No. 1.6e-32;
 Matches 83; Conservative 48; Mismatches 62; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGTLVGRRAQDPDLGNALMAYSLIDGSGSEAFSISTDLQGRGLLT 60
 Db 271 STYQFAPASTPDPDSIGRIKANDADVDEMAEISITGDSYDMFGITTDQTOEGIIIT 330
 QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPFKDVASVAVQADPEPPAFQAAYHL 120
 Db 332 LRKPLDFEETKSYTLKDEANVHIDPFRSGRPFKDTAVKIVVEDADEPVSSTYLL 391
 QY 121 TVPENKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFSTIQEEGTHTAAPLDREA 180
 Db 392 EVKEDVPINSVIGQVATADPDIAKPNVKSVDHRHTDMDEVFNINSNGSIFTSKTLREL 450
 QY 181 RAMHNTLVATLTEL 193
 Db 451 LHMHNTIVATLTEL 463

RESULT 9
 150180
 C/Species: Gallus gallus (chicken)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C/Accession: U150180
 R/Nakagawa, S.; Takeichi, M. Development 121, 1321-1332, 1995
 A/Title: Neural crest cell-cell adhesion controlled by sequential and subpopulation-spe

A:Reference number: 150178; MUID:95309115; PMID:7540531
A:Accession: 150180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-785 <N>
A:Cross-references: UNIPROT:Q90763; GB:D42150; NID:9868000; PIDN:BA07721.1; PID:9868001
C:Superfamily: cadherin; cadherin repeat homology
F:156-262/Domain: cadherin repeat homology <CDH>

Query Match 45.3%; Score 448; DB 2; Length 785;
Best Local Similarity 45.3%; Pred. No. 1.8e-31;
Matches 86; Conservative 38; Mismatches 66; Indels 0; Gaps 0;

QY 3 YQFSVETAGPCTLVGRIRADDPDLGNALMAYSLIDEGSEAFSISTDLQGRGLTVR 62
DB YQYVPESELPLASVAVAKKADADVGNAMERKIVGDEGLGVFKISVDKDTQEGIIITQ 326
QY 63 KPLDFESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRVAVQDAPPEPAFTQAAYHLTV 122
DB KELDFEAKTSTTLRIEAMNAHVDPRLSLGPFDMTVKXIVEDVDEPPVFTSRILSVV 386
QY 123 PENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARA 182
DB 387 SEAKVGTIIGTVAAHPDASNSPVRYSIDRNTDLERYFNIDANSGVITTAKSIDRETV 446
QY 183 WHNLTVALTEL 192
DB 447 WHNLTVALTEL 456

RESULT 10
G02678
cadherin-14 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02678
R:Shibata, T.; Shimoyama, Y.; Gotch, M.; Hirohashi, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01584
A:Accession: G02678
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <SH1>
A:Cross-references: UNIPROT:Q13634; EMBL:U59325; NID:91389852; PIDN:AA02933.1; PID:9138
F:162-268/Domain: cadherin repeat homology <CDH>

Query Match 42.5%; Score 421; DB 2; Length 790;
Best Local Similarity 43.5%; Pred. No. 4.3e-29;
Matches 83; Conservative 39; Mismatches 69; Indels 0; Gaps 0;

QY 3 YQFSVETAGPCTLVGRIRADDPDLGNALMAYSLIDEGSEAFSISTDLQGRGLTVR 62
DB YQYVPESELPLASVAVAKKADADVGNAMERKIVGDEGLGVFKISVDKDTQEGIIITQ 326
QY 63 KPLDFESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRVAVQDAPPEPAFTQAAYHLTV 122
DB KELDFEAKTSTTLRIEAMNAHVDPRLSLGPFDMTVKXIVEDVDEPPVFTSRILSVV 386
QY 123 PENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARA 182
DB 387 SEAKVGTIIGTVAAHPDASNSPVRYSIDRNTDLERYFNIDANSGVITTAKSIDRETV 446
QY 183 WHNLTVALTEL 192
DB 447 WHNLTVALTEL 456

RESULT 11
I51638
F:cadherin - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: I51638; S55391
R:Espeseth, A.; Johnson, E.; Kintner, C.
Mol. Cell. Neurosci. 6, 199-212, 1995
A:Title: Xenopus F-cadherin, a novel member of the cadherin family of cell adhesion mol
A:Reference number: I51638; MUID:96039533; PMID:7496627
A:Accession: I51638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-790 <ESP>
A:Cross-references: UNIPROT:Q91838; EMBL:X85330; NID:9854634; PIDN:CA59679.1; PID:98546
C:Superfamily: cadherin; cadherin repeat homology
F:161-267/Domain: cadherin repeat homology <CR2>

Query Match 42.5%; Score 421; DB 2; Length 790;
Best Local Similarity 44.0%; Pred. No. 4.3e-29;
Matches 84; Conservative 37; Mismatches 70; Indels 0; Gaps 0;

QY 3 YQFSVETAGPCTLVGRIRADDPDLGNALMAYSLIDEGSEAFSISTDLQGRGLTVR 62
DB YQYVPESELPLASVAVAKKADADVGNAMERKIVGDEGLGVFKISVDKDTQEGIIITQ 326
QY 63 KPLDFESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRVAVQDAPPEPAFTQAAYHLTV 122
DB KELDFEAKTSTTLRIEAMNAHVDPRLSLGPFDMTVKXIVEDVDEPPVFTSRILSVV 386
QY 123 PENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARA 182
DB 387 SEAKVGTIIGTVAAHPDASNSPVRYSIDRNTDLERYFNIDANSGVITTAKSIDRETV 446
QY 183 WHNLTVALTEL 192
DB 447 WHNLTVALTEL 456

RESULT 12
I59372
cadherin 12 - human
N:Alternate names: Br-cadherin
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I59372
R:Seftig, S.; Bruno, S.; Scharf, J.M.; Wang, C.H.; Vitale, E.; Gilliam, T.C.; Kunkel, L.N.
Proc. Natl. Acad. Sci. U.S.A. 92, 3702-3706, 1995
A:Title: Expressed cadherin pseudogenes are localized to the critical region of the spl
A:Reference number: I59372; MUID:95249541; PMID:7731968
A:Accession: I59372
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM
A:Molecule type: mRNA
A:Residues: 1-794 <RBS>
A:Cross-references: UNIPROT:P55289; GB:L33477; NID:9793942; PIDN:AA048539.1; PID:9793942
C:Genetics:
A:Gene: GDB:CDH12
A:Cross-references: GDB:596324
A:Map position: SP13-5P14
C:Superfamily: cadherin; cadherin repeat homology
C:Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F:157-160/Domain: cadherin repeat homology <CR1>
F:163-268/Domain: cadherin repeat homology <CR2>
F:272-384/Domain: cadherin repeat homology <CR3>
F:387-489/Domain: cadherin repeat homology <CR4>
F:491-601/Domain: cadherin repeat homology <CR5>
F:610-637/Domain: transmembrane #status predicted <TM>
F:638-794/Domain: intracellular #status predicted <INT>

Query Match 41.5%; Score 411; DB 2; Length 794;
Best Local Similarity 40.4%; Pred. No. 3.3e-28;
Matches 78; Conservative 51; Mismatches 64; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPCTLVGRIRADDPDLGNALMAYSLIDEGSEAFSISTDLQGRGLTV 60
DB 272 SLVQSVETAGPCTLVGRIRADDPDLGNALMAYSLIDEGSEAFSISTDLQGRGLTV 60
QY 61 VRKPLDFESQRSYSPFEVATNTLIDPAYLRGPFKDVASVRVAVQDAPPEPAFTQAAYHL 120

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Db      332 LKKLEDEFTKAYFKVDASNLHIDRPHSAGPFDATATKISVLVDDEPVSFKPLTYM 391
      121 TVPENKAPGLVGOISADLDSFASPIRYSILPHSDPERCFSIQPEEGITHTAAPLDREA 180
      392 EYEDTIVGTLIGAVTQGLDVLGSSAVRIFYIDWSSDSDSYFTIDNGEGTATNBLDRRES 451
Qy      181 RAMNHLTVLATEL 193
      452 TAQNFESIASKV 464

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RESULT 13

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IUFHUCS
caderlin 5 precursor - human
N/Alternate names: 784 antigen; cadherin, endothelial-specific; VE-cadherin
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: S49893; S24305; A43418
R/Breviarlo, F.; Cavada, L.; Conada, M.; Martin-Padura, I.; Golay, J.; Introna, M.; Lamp
submitted to the EMBL Data Library, June 1994
A/Description: Molecular and functional properties of VE-cadherin (784/cadherin-5) a nov
A/Reference number: S49893
A/Accession: S49893
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-784 <BR>
A/Cross-references: UNIPROT:P33151, EMBL:X79981, NID:G599833, PIDN:CA456306.1, PID:G5998
R/Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A/Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A/Reference number: S24305; MUID:91283540; PMID:2059658
A/Accession: S24305
A/Molecule type: mRNA
A/Residues: 5-516, 1, 518-784 <SUZ>
A/Cross-references: EMBL:X59796; NID:G639976; PIDN:CA42468.1; PID:G29593
R/Lampugnani, M.G.; Resnati, M.; Raiteri, M.; Pigott, R.; Plascance, A.; Houen, G.; Ruco
J. Cell Biol. 118, 1511-1522, 1992
A/Title: A novel endothelial-specific membrane protein is a marker of cell-cell contacts
A/Reference number: A43418; MUID:92394977; PMID:1522121
A/Accession: A43418
A/Molecule type: protein
A/Residues: 48-60, 'X', 62, 'X', 64, 108-116, 'X', 118-123, 237-238, 'X', 240, 'X', 242-252, 'X', 254
A/Experimental source: cultured endothelial cells
A/Note: sequence extracted from NCBI backbone (NCBI:P:113040, NCBI:P:113045, NCBI:P:113047,
C/Comment: Cadherins mediate calcium-dependent intercellular adhesion, and are thought t
C/Genetics:
A/Gene: GDB:CDHS
A/Cross-references: GDB:134230; OMTM:601120
A/Map position: 16q22.1-16q22.1
C/Superfamily: cadherin; cadherin repeat homology
C/Keywords: calcium binding; cell adhesion; duplication; glycoprotein; transmembrane pro
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-47/Domain: propeptide #status predicted <PRO>
F/48-784/Product: cadherin 5 #status predicted <MAT>
F/48-593/Domain: extracellular #status predicted <EXT>
F/50-151/Domain: cadherin repeat homology <CR1>
F/154-258/Domain: cadherin repeat homology <CR2>
F/261-372/Domain: cadherin repeat homology <CR3>
F/375-479/Domain: cadherin repeat homology <CR4>
F/481-587/Domain: cadherin repeat homology <CR5>
F/594-620/Domain: transmembrane #status predicted <TM>
F/621-784/Domain: intracellular #status predicted <INT>
F/736-753/Region: serine-rich
F/61, 112, 157, 362, 442, 523, 535/Binding site: carbohydrate (asn) (covalent) #status predict

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Query Match      31.8%; Score 314.5; DB 1; Length 784;
Best Local Similarity 41.1%; Pred No. 1e-19;
Matches 79; Conservative 26; Mismatches 82; Indels 5; Gaps 4;
3 YQFSVETAGPGTIVGRIPAOQDPIGDNNALMAYSLIDEGSFAFSISFDLQGRDGLTVR 62
263 YFVVEDETRVGTSGSLFVEDDEPQNMRTKYSITLKGVDQAFITENPAHNEGIIKPM 322

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Qy      63 KPLDESQSRYSFRVATNTLIDPXYLRGPFKVAVSRVAVQAPPAFAFQAAYHTV 122
      322 KPLDEYVYIQQSYFVTEADPTDLRYM-SPPAGNPAQVIINTVDDEPPIRQGPYHQL 381
      123 PEN-KAPGTLVGOISADLDSFASPIRYSILPHSDPERCFSIQPEEGITHTAAPLDREAR 181
      382 KENQKKP--LIGTVLAMPDPDARHSIGYSIRTSKGGFFRV-TKKGDIYNEKEDREYV 438
Qy      182 AMNHLTVLATEL 193
      439 FWNHLTVLAEKEL 450

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RESULT 14

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IUFHFM
caderlin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 16-Feb-1997
C/Accession: A41087; B41087
R/Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biesemann, H.; Bryant, P.J.; Goodman, C.S.
Cell 67, 853-868, 1991
A/Title: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadh
A/Reference number: A41087; MUID:92069752; PMID:1959133
A/Accession: A41087
A/Molecule type: mRNA
A/Residues: 143-485, 1279-5147 <MAH>
A/Cross-references: GB:M80537
A/Accession: B41087
A/Molecule type: DNA
A/Residues: 1-142, 487-1278 <MA2>
A/Cross-references: GB:M80537
A/Note: 1229-Gly and 1233-Ser were also found
C/Genetics:
A/Gene: fat
A/Cross-references: FlyBase:FBgn001075
C/Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homolog
C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F/1-35/Domain: signal sequence #status predicted <SIG>
F/36-5147/Product: cadherin-related tumor suppressor #status predicted <MAT>
F/36-483/Domain: extracellular #status predicted <EXT>
F/51-156/Domain: cadherin repeat homology <CR1>
F/159-270/Domain: cadherin repeat homology <CR2>
F/271-382/Domain: cadherin repeat homology <CR3>
F/390-494/Domain: cadherin repeat homology <CR4>
F/497-599/Domain: cadherin repeat homology <CR5>
F/602-708/Domain: cadherin repeat homology <CR6>
F/718-822/Domain: cadherin repeat homology <CR7>
F/831-942/Domain: cadherin repeat homology <CR8>
F/948-1049/Domain: cadherin repeat homology <CR9>
F/1052-1153/Domain: cadherin repeat homology <CR10>
F/1156-1278/Domain: cadherin repeat homology <CR11>
F/1281-1384/Domain: cadherin repeat homology <CR12>
F/1387-1489/Domain: cadherin repeat homology <CR13>
F/1492-1601/Domain: cadherin repeat homology <CR14>
F/1607-1713/Domain: cadherin repeat homology <CR15>
F/1717-1823/Domain: cadherin repeat homology <CR16>
F/1826-1922/Domain: cadherin repeat homology <CR17>
F/1925-2021/Domain: cadherin repeat homology <CR18>
F/2028-2167/Domain: cadherin repeat homology <CR19>
F/2169-2278/Domain: cadherin repeat homology <CR20>
F/2281-2384/Domain: cadherin repeat homology <CR21>
F/2387-2491/Domain: cadherin repeat homology <CR22>
F/2494-2586/Domain: cadherin repeat homology <CR23>
F/2599-2703/Domain: cadherin repeat homology <CR24>
F/2707-2810/Domain: cadherin repeat homology <CR25>
F/2813-2913/Domain: cadherin repeat homology <CR26>
F/2915-3013/Domain: cadherin repeat homology <CR27>
F/3014-3124/Domain: cadherin repeat homology <CR28>
F/3127-3229/Domain: cadherin repeat homology <CR29>
F/3232-3334/Domain: cadherin repeat homology <CR30>
F/3337-3439/Domain: cadherin repeat homology <CR31>
F/3442-3545/Domain: cadherin repeat homology <CR32>

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F:3548-3651/Domain: cadherin repeat homology <C32>
F:3654-3756/Domain: cadherin repeat homology <C33>
F:3954-4010/Domain: EGF homology <EG1>
F:4017-4048/Domain: EGF homology <EG2>
F:4056-4089/Domain: EGF homology <EG3>
F:4096-4127/Domain: EGF homology <EG4>
F:4584-4609/Domain: transmembrane #status predicted <TM>
F:4610-5147/Domain: intracellular #status predicted <INT>

Query Match 23.2%; Score 229.5; DB 1; Length 5147;
Best Local Similarity 33.5%; Pred. No. 3.7e-11;
Matches 64; Conservative 28; Mismatches 84; Indels 15; Gaps 7;

QY 3 YQFSVETAGPGTLVGRADPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLTVRKPLDPESOR 62
DB 3234 YQVTPENEPVSGTILTVGATDDDTGPMKRYISGNGNRQDSVDE---RTGGIVIQ 3289
QY 63 KPLDPESORSYSPFEVATNTLIDPAYLRGPFKDVASVAVQDAPE-PPAFTQAAYHLT 121
DB 3290 QQLDYDLIQEYHNI---TVQDLGY--HPLSSVAMLTITLTDVNDNPPVFNHKEYHCY 3342
QY 122 VPENKAPGTLVGOISADLDSPASP-IRYSILPHSDPERCFSTQPE-EGTHTAAPLDRE 179
DB 3343 IPENKPVGTFFQAHADKDSFKNAIHYAFL-SGPDRHFFIMQSGNTISSAVSFDYE 3401
QY 180 ARAWHNLTVLA 190
DB 3402 ERRITVTLQIXA 3412

RESULT 15
G02878
C:cdherin-15 precursor - human
N:Alternate names: M-cadherin; myotubule cadherin
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02878
R:Shimoyama, Y
submitted to GenBank, February 1996
A:Reference number: H01775
A:Accession: G02878
A:Status: preliminary; translated from GB/EMBL/DDbJ
A:Molecule type: mRNA
A:Residues: 1-814 <SH1>
A:Cross-references: UNIPROT:P55291; GB:D83542; NID:g1208423; PIDN:BAI2012.1; PID:g12084
C:Genetics:
A:Gene: GDB:CDH15; CDH14; CDH3
A:Cross-references: GDB:391031; OMIM:114019
A:Map position: 16q22.1-16q22.1
C:Superfamily: cadherin; cadherin repeat homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:155-260/Domain: cadherin repeat homology <CDH>

Query Match 22.0%; Score 218; DB 2; Length 814;
Best Local Similarity 34.7%; Pred. No. 3.5e-11;
Matches 66; Conservative 24; Mismatches 82; Indels 18; Gaps 7;

QY 14 GTLVGRRAQDPDL--GDNALMAYSLIDEGSEAFSISTDLQGRDGLTVRKPLDPESOR 71
DB 275 GVDVGRLEVDKDRDPGSPNVAAPFTILEGDPGQFTIRDPKTNKEGLSIVKALDYSCS 334
QY 72 SYSPFEVATNTL-IDPAYLR--RGPFKDVASVAVQDAPEPPAFTQAAYHLTVPENKAP 128
DB 335 HYEIKVSVQNEAPLQAAALAEARGQ---AKAVVHVQDNEPVPFQENPLRTSLAEGAP 390
QY 129 GTLVGOISADLDSPASPISYSLPHSDPERCFSTQPEEGTHTAAPLDREARA 182
DB 391 GTLVAVTFSARDPTEQLQ-RLSYSKDYDPEDWLQVDAATGRIGTQHVLSPASPFK--GG 447
QY 183 WHNLTVLATE 192
DB 448 WYRAIVLAQD 457

Search completed: December 8, 2004, 10:27:09
Job time : 16.6086 secs

GenCore version 5.1.6 ..
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 77.3595 Seconds
(without alignments)
1435.471 Million cell updates/sec

Title: US-09-788-051-15
Perfect score: 990
Sequence: 1 SLQGSVETAGBGLVGR.....APLDREARAHNLTVLATEL 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	990	100.0	370	2	Q66T00	Q66T00 homo sapien
2	990	100.0	493	2	Q96L07	Q96L07 homo sapien
3	990	100.0	819	1	Q66D_HUMAN	Q66D_HUMAN homo sapien
4	906	91.5	781	2	Q6PEX6	Q6PEX6 mus musculus
5	906	91.5	781	2	AAH57373	AAH57373 mus musculus
6	540	54.5	796	2	Q96CZ9	Q96CZ9 homo sapien
7	537	54.2	796	1	CADB_HUMAN	P55287 homo sapien
8	532	53.7	796	1	CADB_MOUSE	P55288 mus musculus
9	532	53.7	796	2	Q6C7Q6	Q6C7Q6 mus musculus
10	528	53.3	799	1	CADB_HUMAN	P55286 homo sapien
11	527	53.2	716	2	Q6C3T5	Q6C3T5 mus musculus
12	527	53.2	716	2	Q8C4J9	Q8C4J9 mus musculus
13	527	53.2	716	2	AAH57581	AAH57581 mus musculus
14	527	53.2	754	2	Q6BRK4	Q6BRK4 mus musculus
15	527	53.2	799	1	CADB_MOUSE	P97291 mus musculus
16	522	52.7	799	1	CADB_RAT	O54800 ratius norvici
17	519	52.4	792	1	CADB_CHICK	O93319 gallus galli
18	510.5	51.6	508	2	Q6PANA4	Q6PANA4 mus musculus
19	510.5	51.6	508	2	AAH6200	AAH6200 mus musculus
20	503	50.8	794	2	Q93Z64	Q93Z64 xenopus laevis
21	492	49.7	519	2	Q904Z5	Q904Z5 brachydanio
22	485	49.0	789	1	CAD6_RAT	P55280 ratius norvici
23	484	48.9	790	1	CAD6_HUMAN	P55285 homo sapien
24	481	48.6	789	1	CAD6_HUMAN	Q9UL14 homo sapien
25	467	47.2	790	1	CAD6_MOUSE	P97336 mus musculus
26	463	46.8	788	1	CAD6_HUMAN	Q9Y6M8 homo sapien
27	460	46.5	790	1	CAD6_CHICK	Q90762 gallus galli
28	459	46.4	788	2	Q80MS7	Q80MS7 mus musculus
29	459	46.4	788	2	Q8V168	Q8V168 mus musculus
30	459	46.4	788	2	AAH62962	AAH62962 mus musculus
31	457	46.2	789	1	CADA_CHICK	P79395 gallus galli

33	448	45.3	551	2	Q8AMN	Q8AW2	gallus gall
32	448	45.3	785	1	CAD7 CHICK	Q9W763	gallus galli
33	448	45.3	792	2	Q9PFS0	Q9H60	xenopus lae
34	445	44.9	792	1	CADK HUMAN	Q9H65	homo sapien
35	444	44.8	801	1	Q9PFS1	Q9H61	xenopus lae
36	444	44.5	792	2	Q9PFS1	Q9H61	xenopus lae
37	438	44.2	801	2	Q9Z0M3	Q9Z0M3	mus muscul
38	436	44.0	630	2	Q81Y78	Q81Y78	homo sapien
39	436	44.0	785	1	CAD7 HUMAN	Q9U45	homo sapien
40	433	43.7	543	3	Q804X8	Q804X8	gallus galli
41	433	43.7	798	2	Q7ZYV7	Q7ZYV7	gallus galli
42	433	43.7	798	2	Q8QGH3	Q8QGH3	gallus galli
43	431	43.5	785	2	Q8AM92	Q8AM92	mus muscul
44	421	42.5	790	1	CAD1 HUMAN	Q1364	homo sapien
45	421	42.5	790	2	Q91838	Q91838	xenopus lae

ALIGNMENTS

ID	Q86T00	PRELIMINARY;	PRT;	370 AA.
AC	Q86T00;			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Full-length cDNA clone CSDK003Y017 of HeLa cells of Homo sapiens (human) (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Hela cells;			
RL	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.			
RA	Li W.B., Gruber C., Jesse J., Polayes D.;			
RC	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Hela cells;			
RL	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.			
RA	Genoscope;			
RC	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.			
RN	-1- SIMILARITY: Contains 4 cadherin domains.			
CC	EMBL; EX248303; CAD62630.1; ..			
DR	GO; GO:0016020; Cmembrane; IEA.			
DR	GO; GO:0005509; P:calcium ion binding; IEA.			
DR	GO; GO:0007156; P:homophilic cell adhesion; IEA.			
DR	InterPro; IPR002126; Cadherin.			
DR	Pfam; PF00028; Cadherin; 3.			
DR	PRINTS; PR00205; CADHERIN.			
DR	SMART; SM00112; CA; 2.			
DR	PROSITE; PS00232; CADHERIN_1; 1.			
DR	PROSITE; PS0268; CADHERIN_2; 4.			
KW	Calcium; Calcium-binding.			
FT	NON_TER 1			
FT	NON_TER 1			
FT	NON_TER 1			
SEQUENCE	370 AA; 39479 MW; 3996DA4FA84500E0 CRC64;			
Query Match	100.0%; Score 990; DB 2; Length 370;			
Best Local Similarity	100.0%; Pred. No. 1.8e-72;			
Matches 193; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 SLVQSVETAPAGTLVGRLLTAQDDPLGDNLMVYSLIDEGSGAFSLTDLCGRDGLT	60		
DB	23 SLVQSVETAPAGTLVGRLLTAQDDPLGDNLMVYSLIDEGSGAFSLTDLCGRDGLT	82		
QY	61 VKRPJDFESQRSYSPREVEATNTLLDPAYLRGPFKDVASVAVAQDAEPAPFQAAYHL	120		
DB	63 VKRPJDFESQRSYSPREVEATNTLLDPAYLRGPFKDVASVAVAQDAEPAPFQAAYHL	142		
QY	121 TYPENKARETLVGQISADLDSPASPIRYSLTLPSPDERCSIQPEEGTHTAAPLDREA	180		
DB	143 TYPENKARETLVGQISADLDSPASPIRYSLTLPSPDERCSIQPEEGTHTAAPLDREA	202		

QY 181 RAMENLT/LATEL 193
 DB 203 RAMENLT/LATEL 215

RESULT 2

Q96LQ7 PRELIMINARY; PRT; 493 AA.
 AC Q96LQ7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ25193.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RA Niromiya K., Wagatsuma M., Kanda K., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
 RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
 RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
 RA Nagai K., Isegai T., Sugano S.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: Contains 4 cadherin domains.
 DR EMBL; AK057922; BAB71613.1; -
 DR HSSP; P12830.106S.
 DR Genew; HGNC:14265; CDH24.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00205; CADHERIN.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 4.
 DR PROSITE; PS00232; CADHERIN_1; 2.
 DR PROSITE; PS0268; CADHERIN_2; 4.
 DR Calcium; Calcium-binding.
 KW SEQUENCE 493 AA; 53618 MW; 33F10DF3AF09C1E CRC64;

Query Match 100.0%; Score 990; DB 2; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2.5e-72;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLVPSVETAGRTVGRARADDPDLDGNALMAYSLIDGEGSEAFSISTDLQGRGLLT 60
 DB 262 SLVQFSVETAGRTVGRARADDPDLDGNALMAYSLIDGEGSEAFSISTDLQGRGLLT 321
 QY 61 VRKPLDESSQSSYSPVEATNTLIDPAYLRGPFKCVASVAVQDAPPEPFAQAAYHL 120
 DB 322 VRKPLDESSQSSYSPVEATNTLIDPAYLRGPFKCVASVAVQDAPPEPFAQAAYHL 381
 QY 121 TVPENKAPGTLVGQISADIDSPASPRISILPHSPERCFGIQPEEGITHTAPIDREA 180
 DB 382 TVPENKAPGTLVGQISADIDSPASPRISILPHSPERCFGIQPEEGITHTAPIDREA 441
 QY 181 RAMENLT/LATEL 193
 DB 442 RAMENLT/LATEL 454

RESULT 3

CADO HUMAN
 ID_CADO_HUMAN STANDARD; PRT; 819 AA.
 AC Q86UP0; Q86UP1; Q9NT84;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-24 precursor (UNQ2834/PRO34003).

GN Name=CDH24; Synonyms=CDH11L;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND INTERACTIONS WITH
 RP CATEININS.
 RX MEDLINE=22753805; PubMed=12734196; DOI=10.1074/jbc.M304119200;
 RA Katafiasz B.J., Nieman M.T., Wheelock M.J., Johnson K.R.;
 RT "Characterization of cadherin-24, a novel alternatively spliced type
 II cadherin".
 RL J. Biol. Chem. 278:27513-27519 (2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel P.,
 RA Bacon D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh U., Smith V., Stinson U., Yagita A.,
 RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment".
 RL Genome Res. 13:2265-2270 (2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Testis;
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types. Cadherin-24 mediate strong
 CC cell-cell adhesion.
 CC -1 SUBUNIT: Associates with alpha-, beta- and delta-catenins.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1 ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Long form;
 CC IsoId=Q86UP0-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short form;
 CC IsoId=Q86UP0-2; Sequence=VSP_008717;
 CC Name=3;
 CC IsoId=Q86UP0-3; Sequence=VSP_008718, VSP_008719;
 CC Note=No experimental confirmation available.
 CC -1 SIMILARITY: Contains 5 cadherin domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AY260900; AAP20590.1; -
 DR EMBL; AY260901; AAP20591.1; -
 DR EMBL; AY358193; AA088566.1; -
 DR EMBL; AL157477; CAB70758.1; -
 DR PIR; T46418; T46418.
 DR HSSP; P09803.117W.
 DR Genew; HGNC:14265; CDH24.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00205; CADHERIN.
 DR Pfam; PF01043; Cadherin_C_1.
 DR PRINTS; PR00205; CADHERIN.
 DR PROSITE; PS00232; CADHERIN_1; 2.

RA Raahs S.A., Loquellano N.A., Peters G.J., Atkinson R.D., Mullany S.J.,
RA Raahs S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg K.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 5 cadherin domains.
CC EMBL: BC057373; AAH57373.1; .
DR InterPro: IPR002126; Cadherin.
DR InterPro: IPR000233; Cadherin_c_term.
DR Pfam: PF00028; Cadherin; 5.
DR Pfam: PF01049; Cadherin C; 1.
DR Trnadb: PF00206; cadherin; 1.

DR SMART; SM00112; CA: 4.
DR PROSITE; PS00232; CADHERIN_1; 2.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR Cytosium; Calcium binding; Cell adhesion; Transmembrane

Seq	SEQUENCE	/81 AA;	84104 MW;	135960566C93554a Cc064;
Query Match	91.5%;	Score 906;	DB 2;	Length 781;
Best Local Similarity	89.6%;	Pred. No. 2,9E+65;		
Matches 173;	Conservative 11;	Mismatches 9;	Indels 0;	Gaps
QY	1	SLVQFSVETAGBGLVGR	LKAQDPDLGDNALMAYSIIDGSGSEAFSISTDPLQGRDGLLT	
Db	262	SLVQFSVETAGBGLVGR	LKAQDPDLGDNALMAYSIINGGSEVFSISTDSQCDGLLT	
QY	61	VKRPDLFESQRSTISFEVEATNTLLIDPATLRGPFQDVASVYAVQDAEAPPAFQAAHLL		
Db	322	VKRPDLFETRRSTISFEVEATNTLLIDPATLRGPFQDVASVYAVQDAEAPPAFQATVHL		
QY	121	TYEKNAAGTIVQVIAADLDSPAPIRSLIPLHSDPERCSIOPEESTITHTAAPLDSEA		

QY 181 RAHNLTATTEL 193
| | | | : | | |
| | | | : | | |

RESULT 5	
AAH57373	PRELIMINARY; PRT; 781 AA.
ID AAH57373	
AC AAH57373;	
DT 02-MAR-2004 (TEMBRE;. 27, Created)	
DT 02-MAR-2004 (TEMBRE;. 27, Last sequence update)	
DT 02-MAR-2004 (TEMBRE;. 27, Last annotation update)	
DE Catherin-Like 24.	
GN CD824.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX NCBI_Taxid=10090;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=CS7BL/6; TISSUE=Brain;	
RX MEDLINE=22388257; Pubmed=12477932;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	

RA Klausner R.D., Collins F.S., Wagner L., Spennemann C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC057373; AAH57373.1; -
 SQ SEQUENCE 781 AA; 84104 MW; 15996D6E6C9835NA CRC64;
 Query Match 91.5%; Score 906; DB 2; Length 781;
 Best Local Similarity 89.6%; Pred. No. 2, 9e-65;
 Matches 173; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 1 SLVQSVYETAGPGLTVGRRAADPDIGDNALMAYSLIDGEGSEAFSISTDLOGDGLLT 60
 DB 262 SLVQSVYETAGPGLTVGRRAADPDIGDNALMAYSLIDGEGSEAFSISTDLOGDGLLT 321
 QY 61 VRKPLDFESORSYFVREATNTLIDPAYLRGPFKQVAVRVAVQAPPEPAFTQAAYHL 120
 DB 322 VRKPLDFETRSRTFRREANTTLIDPAYLRGPFKQVAVRVAVQAPPEPAFTQAAYHL 381
 QY 121 TPENKAPGTLVQGISADLSDPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
 DB 382 AVENKAPGTLVQGISADLSDPASPIRYSILPHSDPERCFSTIEPDGTRAVLRDREA 441
 QY 181 RAHNLTVLATEL 193
 DB 442 RAHNLTVLATEL 454
 RESULT 6
 Q96CZ9 PRELIMINARY; PRT; 796 AA.
 ID Q96CZ9
 AC Q96CZ9
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cadherin 11, type 2, isoform 1 preproprotein.
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Spennemann C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Heien F.,
 RA Stappleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 DR EMBL: BC013609; AAH13609.1; -
 DR HSSP: P09803; 117W.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; P:calcium ion binding; IEA.
 DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR000233; Cadherin_C-term.
 DR InterPro: IPR001901; SECE.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SMO0112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS0268; CADHERIN_2; 5.
 DR PROSITE: PS01067; SECE SEC6G; UNKNOWN_1.
 DR KX Calcium, Calcium-binding, Cell adhesion, Transmembrane.
 SQ SEQUENCE 796 AA; 87979 MW; 8497F9B834F7547C CRC64;
 Query Match 54.5%; Score 540; DB 2; Length 796;
 Best Local Similarity 51.8%; Pred. No. 2e-35;
 Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;
 QY 1 SLVQSVYETAGPGLTVGRRAADPDIGDNALMAYSLIDGEGSEAFSISTDLOGDGLLT 60
 DB 271 SLVQSVYETAGPGLTVGRRAADPDIGDNALMAYSLIDGEGSEAFSISTDLOGDGLLT 330
 QY 61 VRKPLDFESORSYFVREATNTLIDPAYLRGPFKQVAVRVAVQAPPEPAFTQAAYHL 120
 DB 331 VRKPLDFETRSRTFRREANTTLIDPAYLRGPFKQVAVRVAVQAPPEPAFTQAAYHL 390
 QY 121 TPENKAPGTLVQGISADLSDPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
 DB 391 EVQENKAPGTLVQGISADLSDPASPIRYSILPHSDPERCFSTIEPDGTRAVLRDREA 450
 QY 181 RAHNLTVLATEL 193
 DB 451 RAHNLTVLATEL 463
 RESULT 7
 CADB_HUMAN STANDARD; PRT; 796 AA.
 ID CADB_HUMAN
 AC P55287; O15065; O15066; Q9UG93; Q9UG94;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSP-4).
 GN Name=CDH11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Helmark R.L., St John T., Suzuki S.;
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin";
 RL Cell Adhes. Commun. 2:15-26(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=94216322; PubMed=8163513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Amann E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 RT of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [3]
 RP SEQUENCE OF 269-796 FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.;
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue";
 RL Cell Regul. 2:261-270(1991).
 RN [4]
 RP SEQUENCE OF 600-668 FROM N.A. (ISOFORMS 1 AND 2).
 RA Koels P.F.J., Hogendoorn P.C.W., Boyee J.V.M.G., Van Roy F.;
 RT "Alternative cadherin-11 transcripts encoding truncated adhesion
 RT molecules are detectable in both human cancer and normal cells";
 RL Submitted (ARR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P55287-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P55287-2; Sequence=VSP_000640, VSP_000641;
 CC -1- TISSUE SPECIFICITY: Expressed mainly in brain but also found in
 CC other tissues. Expressed in neuroblasts.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC -----
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L34056; AAA5622.1; -;
 DR EMBL; D21254; BA04798.1; -;
 DR EMBL; D21255; BA04799.1; -;
 DR EMBL; AF060370; AAD27755.1; -;
 DR EMBL; AF060369; AAD27755.1; JOINED.
 DR EMBL; AF060370; AAD27756.1; -;
 DR EMBL; AF060369; AAD27756.1; JOINED.
 DR PIR; A38992; A38992.
 DR HSSP; P09803; 117W.
 DR Genew; HGNC:1750; CDH11.
 DR MIM; 600023; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0007156; P:homophilic cell adhesion; NAS.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C-term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.

DR PRINTS; PR00205; CADHERIN.
 DR SMART; SM00112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS00268; CADHERIN_2; 5.
 KW Alternative splicing; Calcium-binding; Cell adhesion; Glycoprotein;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 22
 FT PROPEP 23 53
 FT CHAIN 54 796
 FT DOMAIN 54 617
 FT TRANSMEM 618 640
 FT DOMAIN 641 796
 FT DOMAIN 54 159
 FT DOMAIN 160 268
 FT DOMAIN 269 383
 FT DOMAIN 384 486
 FT DOMAIN 487 612
 FT CARBOHYD 455 455
 FT CARBOHYD 540 540
 FT VARSPLIC 632 693
 FT
 FT VARSPLIC 694 796
 FT
 FT CONFLICT 271 272
 FT CONFLICT 275 275
 FT CONFLICT 340 340
 FT CONFLICT 373 373
 FT CONFLICT 471 471
 SQ SEQUENCE 796 AA; 88049 MW; 2C67044C78ADB32E CRC64;
 Query Match 54.2%; Score 537; DB 1; Length 796;
 Best Local Similarity 51.6%; Pred. No. 3,5e-35;
 Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;
 QY 2 LYQFSVETAGPGTIVGRLEADPDLDGNALMAVSIIDLGEGSEAFSISTDLOGRDGLTV 61
 DB 272 LYQMSSEAAVYGEVGRKAKDPDIGNGLVTYIVDGDWSEFETIDVETGCVIXL 331
 QY 62 KRPDLPESQKSYSFVYEATNLTIDPAYLRGPFKVAISYRAVQAPPEPATQAAHYHT 121
 DB 332 KRPVPEFETRAYSLKVEANVAHIDKFTSNQFKDTVYKISVEDADEPMTLABSYHE 391
 QY 122 VPENKAPGTLVGQISADLDSPPASPIRYSIILPSPDFPCFSIQPEEGTHTAPLDREAR 181
 DB 392 VQENNAAGTVVGRVAKPDANSPRISIDHTLDLRFITINPDGFKTKKPLDREBT 451
 QY 182 AMNLTVALTEL 193
 DB 452 AMLNITVFAAEI 463
 RESULT 8
 CAD_MOUSE STANDARD; PRT; 796 AA.
 ID CAD_MOUSE
 AC P55288;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-11 precursor (Osteoblast-cadherin) (OB-cadherin) (OSF-4).
 GN Name=Cdh11; Synonyms=Ccd-11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95269886; PubMed=7750649;
 RA Hoffmann I.H., Balling R.;
 RT "Cloning and expression analysis of a novel mesodermally expressed
 RT cadherin.";

RL Dev. Biol. 169:337-346(1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95269887; PubMed=7750650;
 RX Kimura Y., Matsunami H., Inoue T., Shimamura K., Uchida N., Ueno T.,
 RA Miyazaki T., Takeichi M.;
 RT "Cadherin-11 expressed in association with mesenchymal morphogenesis
 in the head, somite, and limb bud of early mouse embryos";
 RL Dev. Biol. 169:347-358(1995).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6; TISSUE=Calvaria;
 RX MEDLINE=94216322; PubMed=816513;
 RA Okazaki M., Takeshita S., Kawai S., Kikuno R., Tsujimura A., Kudo A.,
 RA Aman E.;
 RT "Molecular cloning and characterization of OB-cadherin, a new member
 of cadherin family expressed in osteoblasts";
 RL J. Biol. Chem. 269:12092-12098(1994).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
 RA Diatchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Frange C.,
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.T., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettlem M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smolins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN DEVELOPMENTAL STAGE.
 RP STRAIN=C57BL/6; TISSUE=Testis;
 RX MEDLINE=97033837; PubMed=8879495;
 RA Munro S.B., Blaschuk O.W.;
 RT "A comprehensive survey of the cadherins expressed in the testes of
 fetal, immature, and adult mice utilizing the polymerase chain
 reaction";
 RL Biol. Reprod. 55:822-827(1996).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in osteoblastic cell
 CC lines, precursor cell lines of osteoblasts, and primary
 CC osteoblastic cells from calvaria, as well as in lung, testis, and
 CC brain tissues at low levels.
 CC -1- DEVELOPMENTAL STAGE: In the testis, expression is highest in fetal
 CC gonad and decreases 8-fold in newborn.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC
 CC EMBL: X77557; CAA54674.1; -.

DR EMBL: D31963; BAA06730.1; -.
 DR EMBL: D21253; BAA04797.1; -.
 DR EMBL: BC046314; AAH46314.1; -.
 DR PIR: A53584; A53584.
 DR PIR: I48277; I48277.
 DR PIR: I49556; I49556.
 DR HSP: P09803; I17W.
 DR MGP: MGI:99217; Cdh11.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0005886; C:plasma membrane; IDA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR00233; Cadherin_C-term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PS00205; CADHERIN.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 DR Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM Transmembrane.
 KW
 FT SIGNAL 1 24 Potential.
 FT PROPEP 25 53 Potential.
 FT CHAIN 54 796 Cadherin-11.
 FT DOMAIN 54 617 Extracellular (Potential).
 FT TRANSMEM 618 640 Potential.
 FT DOMAIN 641 796 Cytoplasmic (Potential).
 FT DOMAIN 54 159 Cadherin 1.
 FT DOMAIN 160 268 Cadherin 2.
 FT DOMAIN 269 383 Cadherin 3.
 FT DOMAIN 384 486 Cadherin 4.
 FT DOMAIN 487 612 Cadherin 5.
 FT CARBOHD 455 455 N-linked (GlcNAc...) (Potential).
 FT CARBOHD 540 540 E->D (in Ref. 1).
 FT CARBOHD 462 462 E->D (in Ref. 2).
 FT CONFLICT 589 589 D->N (in Ref. 2).
 FT CONFLICT 655 655 V->M (in Ref. 2).
 FT CONFLICT 751 751 P->Q (in Ref. 1).
 FT CONFLICT 777 777 L->P (in Ref. 2).
 FT CONFLICT 782 782 L->P (in Ref. 2).
 SQ SEQUENCE 796 AA; 88112 MW; 0D584D2464DD529 CRC64;
 Query Match 53.7%; Score 532; DB 1; Length 796;
 Best Local Similarity 50.8%; Pred. No. 8, 3e-35;
 Matches 98; Conservative 42; Mismatches 53; Indels 0; Gaps 0;
 QY 1 SLVPSVETRGPGETLGRRAQPPDGDMAAMAYSLIDEGSGEAFSISTDLCGRDGLT 60
 DB 271 SVYQMSVSEAAVPEEYGVKAKDPDIDGGLVYINVDGDLLEFITTDTYETQDGVK 330
 QY 61 VRKPLDESORSYFVEATNTTLDPAVLRGPFKDVASVAVQDAPPEPAFTQAYHL 120
 DB 331 LKKPVEETKRAYSLKLEAANVHIDPKFISNGPKDVTWKISVEDADEPMLAPYIH 390
 QY 121 TVPNKAPGLTVGQISADIDSPASPIRYSILPHSPDERCFSTQPEEGTHTAPLDREA 180
 DB 391 EVOENAAAGTVGKRVHAKDPDANSPIRYSIDHTDLDREFTINPEDGFIKTKPLDREZ 450
 QY 181 RAMNLTPLATEL 193
 DB 451 TAWLNISVPAEI 463
 RESULT 9
 ID 08C706 PRELIMINARY; PRT; 796 AA.
 AC 08C706;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
 DE enriched library, clone: C530015f15 product: cadherin 11, full insert
 DE sequence.
 GN Name=Cdh11;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.",
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RA The FANTOM Consortium;
 RT "The RIKEN Genome Exploration Research Group Phase I & II Team:
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:553-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama T., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsumaki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imocanti K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai T., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK049652; BAC33860.1; -.
 DR HSSP: P09803; 117W.
 DR MGP: MGI:99217; cdh1.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0005886; C:plasma membrane; IDA.
 DR InterPro: IPR002126; Cadherin.

DR InterPro: IPR002123; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR00205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS00268; CADHERIN_2; 5.
 KW Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 796 AA; 88126 MM; 71963374R2E1BE29 CnC64;
 Query Match 53.7%; Score 532; DB 2; Length 796;
 Best Local Similarity 50.8%; Pred. No. 8.9e-35;
 Matches 98; Conservative 42; Mismatches 53; Indels 0; Gaps 0;
 QY 1 SLVPSVETAGPGTLVGRLEAOPDPLGDNLMVSIIDGSGSEAFSISTDLOGSDGLT 60
 DB 271 SVYQMSVSEAAVGESEVGRVAKDPDIOENGLVYINIVDGDGIELFETITTYETQGVVK 330
 QY 61 VRKPLDFESORSYSFEVATNTLIDPAYLRGPFEDVASVAVQDAPEPPAFTQAAVHL 120
 DB 331 LKKPVPFETKRAYSKIEAAVHIDPKFISNGPFQDTVTKISVEDADEPMPFLAPSYIH 390
 QY 121 TYPENKAGETLVGQISADLDSPASPIRYSILPHSDPERCSIQPEEGTHTAPLDSEA 180
 DB 391 EVQENNAAGTVGRVHAPDPANSPIRYSIDRHTLDLDFITNEDGFITKTPLDNEE 450
 QY 181 RAMNLTVALTEL 193
 DB 451 TAMLNISVPAEI 463
 RESULT 10
 CAD8 HUMAN STANDARD; PRT; 799 AA.
 AC P55286; Q9ULB2;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=CDH8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10861224;
 RA Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.,
 RT "Identification of three human type-II classic cadherins and frequent
 RT heterophilic interactions between different subclasses of type-II
 RT classic cadherins.",
 RL Biochem. J. 349:159-167(2000).
 [2]
 RP SEQUENCE OF 7-799 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95073006; PubMed=7982033;
 RA Tanihara H., Sano K., Heimark R.L., St John T., Suzuki S.,
 RT "Cloning of five human cadherins clarifies characteristic features of
 RT cadherin extracellular domain and provides further evidence for two
 RT structurally different types of cadherin.",
 RL Cell Adhes. Commun. 2:15-26(1994).
 [3]
 RP SEQUENCE OF 294-799 FROM N.A.
 RC TISSUE=Retal brain;
 RX MEDLINE=91283540; PubMed=2059658;
 RA Suzuki S., Sano K., Tanihara H.,
 RT "Diversity of the cadherin family: evidence for eight new cadherins in
 RT nervous tissue.",
 RL Cell Regul. 2:261-270(1991).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.

RESULT 11

08C375
ID 08C375 PRELIMINARY; PRT; 716 AA.
AC 08C375;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:D930046N17 product:cadherin 8, full insert
DE sequence.
DE Name:cdh8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20499374; PubMed=11042259;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsuna T., Tachio H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto S., Matsunoto H., Sakaguchi S., Ikegami T., Harada K.,
RA Fujimoto S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanhiki K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
RA Kato H., Kawai Y., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numata K., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tasami M.,
RA Tsegawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL: AK086711; BAC39724.1; -
 DR HSSP: P15116; INCU.
 DR MGI: MGI:107434; Cdh8.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro: IPR002126; Cadherin.
 DR InterPro: IPR002123; Cadherin_C_term.
 DR Pfam: PF00028; Cadherin_5.
 DR Pfam: PF01049; Cadherin_C_1.
 DR PRINTS: PR0205; CADHERIN.
 DR SMART: SM00112; CA; 5.
 DR PROSITE: PS00232; CADHERIN_1; 3.
 DR PROSITE: PS02668; CADHERIN_2; 5.
 KM Calcium; Calcium-binding; Cell adhesion; Transmembrane.
 SQ SEQUENCE 716 AA; 79149 MW; 58BD598f6638624A CRC64;
 Query Match 53.2%; Score 527; DB 2; Length 716;
 Best Local Similarity 50.3%; Pred. No. 2e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;
 QY 1 SLVPSVETAGPTVIGRLRAOPDGDNAALMYSLIDGSGSAFISTDLOGRDLT 60
 DB 279 SLVPSVETAGPTVIGRLRAOPDGDNAALMYSLIDGSGSAFISTDLOGRDLT 60
 QY 61 VRKPLDSEQSRYSFVEATNTLIDPAYLRGPFKDVASVAVQDAPPEPAFTQAYHL 120
 DB 339 LRKPLDETETKSYLAKYEAANIHDPRFSSKGPKEQATKIVEDDEDFPVSPPYLL 398
 QY 121 TVPENKAPGTLVIGISADLDSPSPRYSLPLPSDEPCSTIOPEEGTHTAPLDREA 180
 DB 399 EVHENAALNSVIGQVTRAPDPTSSPIRFSIDRTDEROFINADGKITLATPDLREL 458
 QY 181 RAWHNLTVLATEL 193
 DB 459 SVWHNITITATEI 471
 RESULT 12
 ID 08C449 PRELIMINARY; PRT; 716 AA.
 AC 08C449;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
 DE library, clone:0630002D14 product:cadherin 8, full insert sequence
 DE (Cdh8 protein).
 GN Name=Cdh8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RL Mech. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RL "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Komno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawat J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi U., Aizawa K., Akimura T., Aikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai Y., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buerow K.H., Scheffer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo K.F., Casavant J.L., Schetz T.E.,
 RA Brownstein W.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.W., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RA Strausberg R.,

Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
CC (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
DR EMBL; AK083092; BAC38758.1; -
DR EMBL; BC057581; AAH57581.1; -
DR HSSP; P15116; INCU.
DR MGD; MGI:107434; Cdh8.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; P:homophilic cell adhesion; IEA.
DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR00233; Cadherin_C-term.
DR Pfam; PF00208; Cadherin; 5.
DR Pfam; PF01049; Cadherin; 1.
DR PRINTS; PR00205; CADHERIN.
DR PROSITE; PS00232; CADHERIN_1; 3.
DR PROSITE; PS50268; CADHERIN_2; 5.
DR Calcium; Calcium-binding; Cell adhesion; Transmembrane.
KW SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;
SQ
Query Match 53.2%; Score 527; DB 2; Length 716;
Best Local Similarity 50.3%; Pred. No. 2e-34;
Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;
QY 1 SLVQFSVETAGPCTVGRVLRADPDIDGNALMAYSILDEGESEAFSITDLCGRGLLT 60
DB 279 SLVHFSVPEVDVLTGTAIGRVKANDQDGENAQSSYDIIDDDGTALFEITSDAQADGVIR 338
QY 61 VRKPLDPESSQSYSFREYEAATNTLLIDPAYLRGPFKDVASRVAVQADAPDPAPFTQAAYHL 120
DB 339 LRKPLDPETKKSYTLKVEANINHIDPFSSRGPFKDTATYKIVEDADEPVSSTYLL 398
QY 121 TVPENKAPGTLVGQISADLDSPPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
DB 399 EVHENAALNSVIGQVTARDPDITSSPIRFSIDRHTLERQFINADDKITLATPDLREL 458
QY 181 RAMHNLTVLATEL 193
DB 459 SWMHNTITIAETI 471
DB
RESULT 13
AAH57581 PRELIMINARY; PRT; 716 AA.
ID AAH57581; TISSUE=Brain;
AC AAH57581; TISSUE=Brain;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Cdh8 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marx M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Strausberg R.;
RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057581; AAH57581.1; -
KW SEQUENCE 716 AA; 79145 MW; 976FF5D845F938BD CRC64;
SQ
Query Match 53.2%; Score 527; DB 2; Length 716;
Best Local Similarity 50.3%; Pred. No. 2e-34;
Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;
QY 1 SLVQFSVETAGPCTVGRVLRADPDIDGNALMAYSILDEGESEAFSITDLCGRGLLT 60
DB 279 SLVHFSVPEVDVLTGTAIGRVKANDQDGENAQSSYDIIDDDGTALFEITSDAQADGVIR 338
QY 61 VRKPLDPESSQSYSFREYEAATNTLLIDPAYLRGPFKDVASRVAVQADAPDPAPFTQAAYHL 120
DB 339 LRKPLDPETKKSYTLKVEANINHIDPFSSRGPFKDTATYKIVEDADEPVSSTYLL 398
QY 121 TVPENKAPGTLVGQISADLDSPPASPIRYSILPHSDPERCFSTIQPEEGTHTAAPLDREA 180
DB 399 EVHENAALNSVIGQVTARDPDITSSPIRFSIDRHTLERQFINADDKITLATPDLREL 458
QY 181 RAMHNLTVLATEL 193
DB 459 SWMHNTITIAETI 471
DB
RESULT 14
Q8BRK4 PRELIMINARY; PRT; 754 AA.
ID Q8BRK4;
AC Q8BRK4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830083P13 product:cadherin 8, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;

RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Cortex;
 RX MEDLINE=20510913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system 384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Cortex;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai U., Kohji Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Maruyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohata N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sato K., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 DR EMBL; AK044046; BAC31751.1; -.
 DR HSSP; P15116; INCT.
 DR GO; GO:0016020; C:membrane, IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0007156; P:homophilic cell adhesion; IEA.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KX Calcium-binding; Cell adhesion; Transmembrane.
 KW SEQUENCE 754 AA; 83624 MW; 149C3C70D3F21568 CRC64;
 SQ
 Query Match 53.2%; Score 527; DB 2; Length 754;
 Best Local Similarity 50.3%; Pred. No. 2, 3e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

DB 459 SYMNITITATEI 471
 RESULT 15
 CAD8_MOUSE STANDARD; PRI; 799 AA.
 ID CAD8_MOUSE
 AC P97291;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cadherin-8 precursor.
 GN Name=Cad8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster / NIH;
 RX MEDLINE=97174321; PubMed=9022055;
 RA Korematsu K., Redies C.;
 RT "Restricted expression of cadherin-8 in segmental and functional
 RT subdivisions of the embryonic mouse brain.";
 RL Dev. Dyn. 208:178-189 (1997).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 CC They preferentially interact with themselves in a homophilic
 CC manner in connecting cells; cadherins may thus contribute to the
 CC sorting of heterogeneous cell types.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 5 cadherin domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; X55600; CAA64857.1; -.
 DR HSSP; P09803; IITW.
 DR MGD; MGI:107434; Cdh8.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000233; Cadherin_C_term.
 DR Pfam; PF00028; Cadherin_5.
 DR Pfam; PF01049; Cadherin_C_1.
 DR PRINTS; PRO0205; CADHERIN.
 DR SMART; SMO0112; CA; 5.
 DR PROSITE; PS00232; CADHERIN_1; 3.
 DR PROSITE; PS0268; CADHERIN_2; 5.
 DR KX Calcium-binding; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 29
 FT PROPEP 30 61 Potential.
 FT CHAIN 62 799 Cadherin-8.
 FT DOMAIN 62 621 Extracellular (Potential).
 FT TRANSMEM 622 642 Potential.
 FT DOMAIN 643 799 Cytoplasmic (Potential).
 FT DOMAIN 62 167 Cadherin 1.
 FT DOMAIN 168 276 Cadherin 2.
 FT DOMAIN 277 391 Cadherin 3.
 FT DOMAIN 392 494 Cadherin 4.
 FT DOMAIN 495 616 Cadherin 5.
 FT CARBOHYD 188 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 473 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 544 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 799 AA; 88200 MW; 0E35FEAD563C7F76 CRC64;
 Query Match 53.2%; Score 527; DB 1; Length 799;
 Best Local Similarity 50.3%; Pred. No. 2, 3e-34;
 Matches 97; Conservative 41; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRLAODPDIGDNNALMAYSLDGESEAFSISTDLQGRDGLLT 60
Db 279 SLVHFSVPEBVDVLGTAIGRVXANDQDIGENAOSSYDIIDGDTALFEITSDAQODGVIR 338
QY 61 VRKPLDFESORSVSERVBATNTLIDPAYLRGPERKDVASVRAVODAPPEPAFTQAAYHL 120
Db 339 LRKPLDFETKKSITLKEBANIRHIDRFSSRGPPKDTATVKIVVEDADBPVFSPTYL 398
QY 121 TVPENKAPGTLVQISAADLSPASPIRYSILPHSDPERCFSIQPEGTIHTAAPLDREA 180
Db 399 EVHENAALNSVICQVTARDPDITSSPIRFSIDRHTDLERQFNINADDGKITLATPLDREL 458
QY 181 RAHNLTVLATEL 193
Db 459 SVMHNTTILATEI 471

Search completed: December 8, 2004, 10:24:41
Job time : 78.3595 secs

CC protein and the DNA sequence which encodes it. Cadherins are a family of
CC transmembrane proteins which share a common cadherin domain in their
CC extracellular region. The extracellular portion mediates homotypic cell-
CC cell adhesion that is calcium dependent. Modulators of the protein of the
CC invention may have cytostatic or osteopathic activity. The invention may
CC allow development of therapeutic useful for the treatment of diseases
CC such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC invention may also be useful as markers for prognosis of metastatic
CC tumours. The present sequence is that of a peptide fragment of the human
CC secreted cadherin-like protein which was used during the exemplification
CC of the invention.

SQ Sequence 193 AA;

Query Match 100.0%; Score 990; DB 7; Length 193;
Best Local Similarity 100.0%; P-Id. No. 7, 5e-101;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPTLVGRRLRAQPPDGDNALMAYSLIDEGSEAFSISTDLGGRLTLT 60
Db 1 SLVQSVETAGPTLVGRRLRAQPPDGDNALMAYSLIDEGSEAFSISTDLGGRLTLT 60
QY 61 VRKPLDESGRSYFVEATNTLIDPAYLRGPKQVAVVAVQDAPEPPAFTQAAYHL 120
Db 61 VRKPLDESGRSYFVEATNTLIDPAYLRGPKQVAVVAVQDAPEPPAFTQAAYHL 120
QY 121 TVPENKAPGTLVQGISADLDSPASPTRYSLPHSDPERCFSTOPEEGTHTAPLDREA 180
Db 121 TVPENKAPGTLVQGISADLDSPASPTRYSLPHSDPERCFSTOPEEGTHTAPLDREA 180
QY 181 RAWENLTVALTEL 193
Db 181 RAWENLTVALTEL 193

RESULT 2

AD116946

AD116946 standard; protein; 493 AA.

AD116946;

15-APR-2004 (first entry)

Human NOVX protein homologue SeqID 482.

human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
inflammation; autoimmune disorder; allergy; blood disorder;
acquired immunodeficiency syndrome; AIDS; obesity; asthma;
immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
Alzheimer's disease; infection; str.

Homo sapiens.

WO200268649-A2.

06-SEP-2002.

31-JAN-2002; 2002WO-US0002785.

31-JAN-2001; 2001US-0265395P.

31-JAN-2001; 2001US-0265412P.

31-JAN-2001; 2001US-0265514P.

31-JAN-2001; 2001US-0265517P.

02-FEB-2001; 2001US-0266466P.

05-FEB-2001; 2001US-0266767P.

07-FEB-2001; 2001US-0266975P.

08-FEB-2001; 2001US-0267459P.

09-FEB-2001; 2001US-0267823P.

15-FEB-2001; 2001US-0268974P.

26-FEB-2001; 2001US-0271664P.

27-FEB-2001; 2001US-0271839P.

27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279883P.
PR 29-MAR-2001; 2001US-0279885P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282929P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312028P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313390P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.
XX Tchervet VT, Spytek KA, Zernusen BD, Patturajan M, Shinkets RA;
XX Li L, Gangoli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
XX Gerlach VV, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
XX Furtak K, Grosse WM, Alsbrook JP, Lepley DM, Rieger DK, Burgess CE;
XX WPI, 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
pharmacogenomics.

Disclosure: SEQ ID NO 482; 1498bp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides
thereof, which have properties related to the stimulation of biochemical
or physiological responses in a cell, tissue, organ or organism.
Specifically, it refers to the use of biologically active fragments for
diagnostic and prognostic assays and furthermore in the treatment of
diverse pathological conditions. The present invention describes novel
human and murine NOVX proteins, as well as methods to modulate their
expression using antisense oligos, ribozymes and peptide nucleic acids.
The NOVX polypeptides, polynucleotides and antibodies are useful in
treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
atherosclerosis, cancer and diabetes. Furthermore, they may be used in
treating or preventing diseases such as inflammation, autoimmune
disorders, allergies, blood disorders, acquired immunodeficiency syndrome
(AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy

CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytoskeletal, cardiant, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiaesthetic, neurotropic, antiaerobic, hepatotropic,
 CC neuroprotective, neurotropic, antibacterial, vituicide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein
 CC of the invention.

XX Sequence 493 AA;

SO Query Match 100.0%; Score 990; DB 5; Length 493;

Best Local Similarity 100.0%; Pred. No. 2.9e-100;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
 DB 262 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
 QY 61 VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQADAPPPAFTQAAYHL 120
 DB 322 VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQADAPPPAFTQAAYHL 361
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 441
 QY 181 RAMENLTVALATEL 193
 DB 442 RAMENLTVALATEL 454

RESULT 3
 ABB53295
 ID ABB53295 standard; protein; 607 AA.

XX ABB53295;

DT 12-FEB-2002 (first entry)

DE Human polypeptide #35.

XX Human; noctropic; neuroprotective; anticonvulsant; antidepressant;
 KW neuroleptic; tranquilizer; antiarrhythmic; cardiant; antiaesthetic;
 KW antiinflammatory; antidiabetic; hepatotropic; vituicide; antidiabetic;
 KW nephrotropic; anorectic; cytoskeletal; vaccine; neurological disease;
 KW cardiovascular disease; respiratory disease; liver disease;
 KW renal disease; skeletal muscle disease; gastrointestinal disease;
 KW placental disease; testicular cancer; male fertility; pancreatic disease.

XX Homo sapiens.

PN WO200181363-A1.

PD 01-NOV-2001.

PT 26-APR-2001; 2001WO-US013360.

XX 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-020336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

XX (SMTK) SMITHKLINE BEECHAM CORP.

XX (SMTK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kadnick KS;
 XX Lai Y, Xie Q;
 XX WPI; 2002-041392/05.

DR N-PSDB; ABA90360.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing
 PT and treating diseases associated the polypeptide, e.g. Alzheimer's
 PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.
 XX Claim 1, Page 106-108; 116pp; English.

XX The invention relates to an isolated polypeptide comprising a 277, 480,
 CC 583, 581, 628, 424, 638, 229, 310, 841, 241, 359, 382, 185, 586, 1026,
 CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255,
 CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as
 CC given in the specification. The polypeptides, modulators of the
 CC polypeptides and antibodies against the polypeptides are useful for
 CC treating diseases such as neurological and psychiatric diseases including
 CC Alzheimer's, paraneoplastic disease, Huntington's disease, myotonic
 CC dystrophy, anorexia and depression; cardiovascular diseases including
 CC congestive heart failure, Hodgkin's disease and myocardial infarction;
 CC respiratory diseases including asthma, chronic obstructive pulmonary
 CC disease, cystic fibrosis and adult respiratory distress syndrome; liver
 CC diseases including hypercholesterolemia, cirrhosis, viral and nonviral
 CC hepatitis, Type II diabetes mellitus, acute tubular necrosis and
 CC renal disease including renal failure, acute tubular necrosis and
 CC glomerulonephritis; skeletal muscle diseases including Duchenne's
 CC disease, hypoglycaemia and obesity; gastrointestinal diseases including
 CC myotonia congenita and intestinal obstruction; lymph diseases including
 CC lymphagiectasia; diseases of placenta including choriocarcinoma; diseases
 CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketoacidosis, Type I and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX Sequence 607 AA;

SO Query Match 100.0%; Score 990; DB 5; Length 607;

Best Local Similarity 100.0%; Pred. No. 3.9e-100;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
 DB 262 SLVQFSVETAGPTLVGRRAQDPDLGNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
 QY 61 VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQADAPPPAFTQAAYHL 120
 DB 322 VRKPLDFESQSYSEFVEATNTLIDPAYLRGPFKDVASVAVQADAPPPAFTQAAYHL 361
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTIHTAAPLDREA 441
 QY 181 RAMENLTVALATEL 193
 DB 442 RAMENLTVALATEL 454

RESULT 4
 ADD29448
 ID ADD29448 standard; protein; 620 AA.

XX ADD29448;

AC ADD29448;

DT 15-JUN-2004 (first entry)

DE Human cadherin-like mature protein.

XX cadherin-like protein; transmembrane protein; cadherin domain;
 KW homotypic cell-cell adhesion; cytoskeletal; osteopetrotic; cancer;
 KW osteoporosis; Paget's disease; osteomalacia; hyperostosis; osteopetrosis;
 KW metastatic tumour; human.

XX Homo sapiens.

OS Homo sapiens.

PN US2003144491-A1.

XX	31-JUL-2003.
XX	
PF	16-FEB-2001; 2001US-00788051.
XX	
XX	03-FEB-2000; 2000US-00496914.
PR	27-FEB-2000; 2000US-00560875.
XX	
PA	(GODBL/) GODBLE S D.
PA	(KUC/) KUO C.
PA	(ARTE/) ARTERBURN M C.
PA	(YEUN/) YEUNG G.
PA	(PALE/) PALENCIA S.
PA	(TANG/) TANG Y T.
PA	(LIUC/) LIU C.
PA	(DRMA/) DRMANAC R T.
XX	
PI	Godbole SD, Kuo C, Arterburn MC, Yeung G, Palencia S, Tang YN,
PI	Liu C, Drmac RT;
XX	
DR	WPI; 2003-829799/77.
XX	
PT	Novel isolated human secreted cadherin-like polypeptide useful for
PT	treating diseases such as cancers, osteoporosis, Paget's disease,
PT	osteomalacia, hyperostosis, osteopetrosis.
XX	
PS	Claim 11; SEQ ID NO 7; 63bp; English.
XX	
CC	This invention relates to a novel isolated human secreted cadherin-like
CC	protein and the DNA sequence which encodes it. Cadherins are a family of
CC	transmembrane proteins which share a common cadherin domain in their
CC	extracellular region. The extracellular portion mediates homotypic cell-
CC	cell adhesion that is calcium dependent. Modulators of the protein of the
CC	invention may have cytosatic or osteoparic activity. The invention may
CC	allow development of therapeutics useful for the treatment of diseases
CC	such as cancers, osteoporosis, Paget's disease, osteomalacia,
CC	hyperostosis and osteopetrosis. The protein and DNA sequence of the
CC	invention may also be useful as markers for prognosis of metastatic
CC	tumours. The present sequence is that of the mature human secreted
CC	cadherin-like protein which was used during the exemplification of the
CC	invention.
XX	
XX	Sequence 620 Aa.
XX	
Query Match	100.0%; Score 990; D8 7; Length 620;
Best Local Similarity	100.0%; Pred. No. 4e-100;
Matches 193; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 SLVQFSVETRAGGTLVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLCGRDGLT 60
DB	246 SLVQFSVETRAGGTLVGRRAQDDPLGDNALMAYSILDGSGSAFSTIDLCGRDGLT 305
QY	61 VRKPLDPESGRSYSPFEVETNTLLIDPAYLRKPFKDVASVVAVQDAPEPPAFTQAAVHL 120
DB	306 VRKPLDPESGRSYSPFEVETNTLLIDPAYLRKPFKDVASVVAVQDAPEPPAFTQAAVHL 365
QY	121 TVENKAPGLTVQGISAADLSDPASPPIRYSILPHSDPERCSIQPEEGTHTAAPLDREA 180
DB	366 TVENKAPGLTVQGISAADLSDPASPPIRYSILPHSDPERCSIQPEEGTHTAAPLDREA 425
QY	181 RAWNLTVALTEL 193
DB	426 RAWNLTVALTEL 438
XX	
RESULT 5	
ADD29445	
ID	ADD29445 standard; protein; 636 Aa.
XX	
AC	ADD29445;
XX	
XX	15-JAN-2004 (first entry)
XX	

Query Match	100.0%; Score 990; DB 7; Length 636;
Best Local Similarity	100.0%; Pred. No. 4.2e-100;
Matches 199; Conservative	0; Mismatches 0; Indels 0; Gaps 0
1	SLYQSVETAGPGTLVGRLLRAQDDPLGDNNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
262	SLYQSVETAGPGTLVGRLLRAQDDPLGDNNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
61	VRKPLDFEQRQSYSRFVENATNTLLDPAIRGPGKDVASRVAVQAPPEPAPTAQAAHL 120
322	VRKPLDFEQRQSYSRFVENATNTLLDPAIRGPGKDVASRVAVQAPPEPAPTAQAAHL 381
121	TYPENKAPGLTVGQISAADLDSPASPIRYSILPHSDERCFSIQPEEGTTHTAAPLDREA 180

Db 382 TYPENKAPGTLVGQISADLDSPAPRIYSILPHSDPERCFSTIQPEEGTIHTAFLDREA 441
 QY 181 RAMNHLTVLATEL 193
 442 RAMNHLTVLATEL 454

RESULT 6
 ID ABB53296 standard; protein; 781 AA.
 ABB53296

AC ABB53296;
 DT 12-FEB-2002 (first entry)

DE Human polypeptide #36.

Human; nocotropic; neuroprotective; anticonvulsant; antidepressant;
 neuroleptic; tranquilizer; antiarrhythmic; cardiac; antidiabetic;
 antiinflammatory; antilipemic; hepatotropic; virucide; antidiabetic;
 nephrotropic; anorectic; cytostatic; vaccine; neurological disease;
 cardiovascular disease; respiratory disease; liver disease;
 renal disease; skeletal muscle disease; gastrointestinal disease;
 placental disease; testicular cancer; male fertility; pancreatic disease.

OS Homo sapiens.
 PN W0200181363-A1.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013360.

PR 27-APR-2000; 2000US-0199963P.

PR 11-MAY-2000; 2000US-0203336P.

PR 25-MAY-2000; 2000US-0207087P.

PR 26-MAY-2000; 2000US-0207546P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdock PR, Rizvi SK, Smith RF, Xiang Z, Kadnick KS,

PI Lai Y, Xie Q.

PT WPI; 2002-041392/05.

DR N-PSDB; ABA90361.

XX Novel polypeptides and polynucleotides useful as a vaccine for preventing

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

PT disease, dyslipidemia, obesity, diabetes, infertility, asthma, amnesia.

CC of testes including testicular cancer, male reproductive diseases
 CC including low testosterone and male infertility; and disease of pancreas
 CC including diabetic ketacidosis, Type 1 and 2 diabetes and obesity. The
 CC present sequence is a polypeptide of the invention

XX Sequence 781 AA;

Query Match 100.0%; Score 990; DB 5; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.6e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIXQSVVETAPGTLVGRTPADPDLDNMLMAYSLIDGSEAFSTLDLGRDGLT 60
 262 SLIQSVVETAPGTLVGRTPADPDLDNMLMAYSLIDGSEAFSTLDLGRDGLT 321
 Db 61 VRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVASVAVADAEPAFTQAAVHL 120
 322 VRKPLDFESQSRYSFVEATNTLIDPAYLRGPFKDVASVAVADAEPAFTQAAVHL 381
 QY 121 TYPENKAPGTLVGQISADLDSPAPRIYSILPHSDPERCFSTIQPEEGTIHTAFLDREA 180
 Db 382 TYPENKAPGTLVGQISADLDSPAPRIYSILPHSDPERCFSTIQPEEGTIHTAFLDREA 441
 QY 181 RAMNHLTVLATEL 193
 442 RAMNHLTVLATEL 454

RESULT 7

AAM48736

ID AAM48736 standard; protein; 781 AA.

AC AAM48736;

DT 28-MAR-2002 (first entry)

DE Human cadherin family member 57805 protein SEQ ID NO 2.

Human; cadherin 57805; osteopathic; hepatotropic; antibacterial;
 antidiabetic; neuroprotective; antiarrhythmic; antineumatic;
 dermatologic; immunosuppressive; antiinflammatory; antipruritic;
 antisthmatic; antiallergic; antileptotic; haemostatic; antipruritic;
 antithyroid; hypotensive; antiarteriosclerotic; cardiac; antiarrhythmic;
 anorectic; immunomodulatory; vasotropic; virucide; cytostatic; liver;
 thrombolytic; analgesic; anabolic; immune disorder; cardiovascular;
 viral; pain; metabolism; osteoporosis; diabetes mellitus; arthritis;
 osteoarthritis; multiple sclerosis; Crohn's disease; asthma; allergy;
 thrombus; inflammation; infection; ischaemia; irritabile bowel syndrome;
 Gene therapy.

OS Homo sapiens.

PN W0200190145-A2.

PD 29-NOV-2001.

PF 18-MAY-2001; 2001WO-US016013.

PR 19-MAY-2000; 2000US-0205674P.

PA (MILL-) MILLENNITUM PHARM INC.

PI Curtis PAU;

PT WPI; 2002-083082/11.

DR N-PSDB; ABA96406, ABA96407.

XX New human cadherin family protein and polynucleotides, useful for

PT diagnosing and treating disorders e.g. obstructive jaundice, multiple

PT sclerostis, encephalomyelitis and atherosclerosis and to identify

PT modulators of therapeutic use.

PS Claim 9; Page 105; 119pp; English.

XX The invention relates to human cadherin family polypeptide designated
 CC 57805 with osteopathic, hepatocytic, antibacterial, antidiabetic,
 CC neuroprotective, antirheumatic, antirheumatic, dermatological,
 CC immunosuppressive, antiinflammatory, antipruritic, antiallergic,
 CC antiallergic, antipruritic, haemostatic, antipruritic, antiallergic,
 CC hypotensive, antidiabetic, antidiabetic, antidiabetic, antidiabetic,
 CC immunomodulatory, vasodilator, cytostatic, thrombolytic,
 CC analgesic and anabolic activity. The 57805 molecules are useful for
 CC diagnosing and treating disorders which include disorders associated with
 CC bone metabolism, immune disorders, cardiovascular disorders, liver
 CC disorders, viral diseases, pain or metabolic disorders. Especially bone
 CC metabolism including osteoporosis, rickets, osteosclerosis, cirrhosis;
 CC immune disorders including autoimmune disease including diabetes mellitus
 CC arthritis, including rheumatoid arthritis and osteoarthritis, multiple
 CC sclerosis, systemic lupus, dermatitis, psoriasis, Crohn's disease,
 CC asthma, thrombocytopenia, Graves' disease, graft-versus-host disease,
 CC allergy, cardiovascular disorders, thrombus, hypertension,
 CC atherosclerosis, arrhythmias and cardiomyopathy; liver disorders,
 CC glycogen storage disease, vascular disorders, chronic heart failure,
 CC portal vein thrombosis, viral diseases; metabolic or pain disorders,
 CC include obesity, anorexia nervosa and diabetes, inflammation, infection
 CC and ischaemia, irritable bowel syndrome. The polynucleotides are also
 CC useful in gene therapy

XX Sequence 781 AA;

Query Match 100.0%; Score 990; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 5, 6e-100; Indels 0; Gaps 0;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLGDNALMAVSTLDEGSEAPSTIDLGRCGLLT 60
 DB 262 SLVQSVETAGPGLVGRRAQDPDLGDNALMAVSTLDEGSEAPSTIDLGRCGLLT 321

QY 61 VRKPLDPSQSRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQDAPPEPPTQAAYHL 120
 DB 322 VRKPLDPSQSRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQDAPPEPPTQAAYHL 381

QY 121 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTIQPEBGTHHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTIQPEBGTHHTAAPLDREA 441

QY 181 RAMNLTIVLATEL 193
 DB 442 RAMNLTIVLATEL 454

RESULT 8

ID ABG34078 standard; protein; 781 AA.

AC ABG34078;

DE 15-JUL-2002 (first entry)

DE Human Pro peptide #49.

KW Human; PRO; secreted protein; transmembrane protein; genetic disorder;

KW tumour; cancer.

OS Homo sapiens.

PN W020022488-A2.

PF 29-AUG-2001; 2001WO-US027099.

PR 01-SEP-2000; 2000US-0229886P.

PR 03-SEP-2000; 2000US-0230621P.

PR 22-SEP-2000; 2000US-0235147P.

PR 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.
 PR 16-JAN-2001; 2001US-0261910P.
 PR 16-JAN-2001; 2001US-0261939P.
 PR 16-JAN-2001; 2001US-0262150P.
 PR 25-JAN-2001; 2001US-0264395P.
 PR 02-FEB-2001; 2001US-0266421P.
 PR 09-FEB-2001; 2001US-0267623P.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 09-MAR-2001; 2001US-0274399P.
 PR 03-APR-2001; 2001US-0280982P.
 PR 04-APR-2001; 2001US-0282129P.
 PR 04-APR-2001; 2001US-0282199P.
 PR 09-MAY-2001; 2001US-0290589P.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021066.
 PR 29-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;

PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;

PI Fong S;

DR WPI: 2002-362426/39.

DR N-PSDB; ABK70009.

PT New PRO polypeptides and polynucleotides encoding the polypeptides, or

PT useful in gene therapy, chromosome identification, tissue typing, or for

PT genetic analysis of individuals with genetic disorders.

PS Claim 11; Fig 98; 218pp; English.

CC This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The invention
 CC also comprises a method for producing the proteins of the invention by
 CC recombinant means and antibodies specific for the protein of the
 CC invention. The antibody may be used for detecting the PRO proteins of the
 CC invention and may be used to modify their activity. Polynucleotides may
 CC be used as hybridisation probes for a cDNA library to isolate the full-
 CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
 CC probes for mapping the gene which encodes that PRO and for genetic
 CC analysis of individuals with genetic disorders, in assays to identify
 CC other proteins or molecules involved in binding reaction, to generate
 CC transgenic animals or knock-out animals which in turn are useful in the
 CC development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides are
 CC useful in gene therapy, and as molecular weight markers for protein
 CC electrophoresis purposes. The sequences may also be used to detect
 CC overexpression on PRO polypeptides in cancerous tumours and for screening
 CC for differentially expressed genes using microarray technology. The
 CC present sequence represents a human PRO protein of the invention

XX Sequence 781 AA;

Query Match 100.0%; Score 990; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 5, 6e-100; Indels 0; Gaps 0;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLGDNALMAVSTLDEGSEAPSTIDLGRCGLLT 60
 DB 262 SLVQSVETAGPGLVGRRAQDPDLGDNALMAVSTLDEGSEAPSTIDLGRCGLLT 321

QY 61 VRKPLDPSQSRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQDAPPEPPTQAAYHL 120
 DB 322 VRKPLDPSQSRYSFRVEATNTLIDPAYLRGPFKDVASRVAVQDAPPEPPTQAAYHL 381

QY 121 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTIQPEBGTHHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTIQPEBGTHHTAAPLDREA 441

QY 181 RAMNLTIVLATEL 193

|||||
442 RAWNTLVATLTEL 454

RESULT 9
AD116606
ID AD116606 standard; protein, 781 AA.

AD116606;

15-APR-2004 (first entry)

Human NOVX protein to treat human pathological conditions SegID142.

human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
inflammation; autoimmune disorder; allergy; blood disorder;
acquired immunodeficiency syndrome; AIDS; obesity; asthma;
immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
cytostatic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
antiaesthetic; nephrotoxic; antiarthritic; hepatocytic;
neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
chromosome mapping; tissue typing; pharmacogenomic.

Homo sapiens.

WO200268649-A2.

06-SEP-2002.

31-JAN-2002; 2002WO-US002785.

31-JAN-2001; 2001US-0265395P.
31-JAN-2001; 2001US-0265412P.
31-JAN-2001; 2001US-0265514P.
31-JAN-2001; 2001US-0265517P.
02-FEB-2001; 2001US-0266406P.
05-FEB-2001; 2001US-0266767P.
07-FEB-2001; 2001US-0266975P.
08-FEB-2001; 2001US-0267057P.
08-FEB-2001; 2001US-0267459P.
15-FEB-2001; 2001US-0268974P.
26-FEB-2001; 2001US-0271664P.
27-FEB-2001; 2001US-0271839P.
27-FEB-2001; 2001US-0271855P.
02-MAR-2001; 2001US-0272788P.
14-MAR-2001; 2001US-0275925P.
14-MAR-2001; 2001US-0275947P.
14-MAR-2001; 2001US-0275950P.
14-MAR-2001; 2001US-0275989P.
15-MAR-2001; 2001US-0276448P.
15-MAR-2001; 2001US-0276450P.
16-MAR-2001; 2001US-0276397P.
16-MAR-2001; 2001US-0276768P.
20-MAR-2001; 2001US-0278652P.
26-MAR-2001; 2001US-0278775P.
26-MAR-2001; 2001US-0278778P.
29-MAR-2001; 2001US-0278822P.
29-MAR-2001; 2001US-0279884P.
30-MAR-2001; 2001US-0280147P.
11-APR-2001; 2001US-0283929P.
11-APR-2001; 2001US-0283983P.
20-APR-2001; 2001US-0285133P.
23-APR-2001; 2001US-0285749P.
03-MAY-2001; 2001US-0288327P.
23-MAY-2001; 2001US-0288504P.
29-MAY-2001; 2001US-0294047P.
30-MAY-2001; 2001US-0294473P.
08-JUN-2001; 2001US-0296964P.

18-JUN-2001; 2001US-0296959P.
19-JUN-2001; 2001US-0299324P.
13-AUG-2001; 2001US-0312020P.
16-AUG-2001; 2001US-0312889P.
16-AUG-2001; 2001US-0312908P.
21-AUG-2001; 2001US-0313390P.
28-AUG-2001; 2001US-0315470P.
31-AUG-2001; 2001US-0316447P.
07-SEP-2001; 2001US-0318115P.
07-SEP-2001; 2001US-0318118P.
12-SEP-2001; 2001US-0318740P.
19-SEP-2001; 2001US-0323379P.
18-OCT-2001; 2001US-0330245P.
18-OCT-2001; 2001US-0330308P.
14-NOV-2001; 2001US-0332701P.

(CURA-) CURAGEN CORP.

Tchernov VT, Spyrek KA, Zerhusen BD, Patrujan M, Shinkets RA;
Li L, Gangoli ER, Padigaru M, Anderson DW, Rastelli L, Miller CE;
Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
Furtak K, Grosse WM, Alsdbrook JP, Lepley DW, Rieger DK, Burgess CE;
WPT; 2002-706998/76.
N-PSDB; AD116605.

New NOVX polypeptides and nucleic acids, useful for preventing or
treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
pharmacogenomics.

Claim 1; SEQ ID NO 142; 1498bp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides
thereof, which have properties related to the stimulation of biochemical
or physiological responses in a cell, tissue, organ or organism.
Specifically, it refers to the use of biologically active fragments for
diagnostic and prognostic assays and furthermore in the treatment of
diverse pathological conditions. The present invention describes novel
human and murine NOVX proteins, as well as methods to modulate their
expression using antisense oligos, ribozymes and peptide nucleic acids.
The NOVX polypeptides, polynucleotides and antibodies are useful in
treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
atherosclerosis, cancer and diabetes. Furthermore, they may be used in
treating or preventing diseases such as inflammation, autoimmune
disorders, allergies, blood disorders, acquired immunodeficiency syndrome
(AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy
and epilepsy. Accordingly, these molecules have many activities including
cytostatic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
antiaesthetic, nephrotoxic, antiarthritic, hepatocytic,
neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
relaxant and anticonvulsant. In addition, they are useful in screening
assays to identify small molecules that modulate or inhibit for example,
neurogenesis, wound healing and angiogenesis. The nucleic acids are also
used as in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. This polypeptide is a human NOVX protein of the
invention.

Sequence 781 AA;

Query Match 100.0%; Score 990; DB 5; Length 781;

Best Local Similarity 100.0%; Pred. No. 5.6e-100; Indels 0; Gaps 0;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGTIGRLRAQDDPLGNALMAYSILIDGESSEAFSITDQGRGLLT 60
DB 262 SLVQFSVETAGPGTIGRLRAQDDPLGNALMAYSILIDGESSEAFSITDQGRGLLT 321
QY 61 VRKPLDFESQRSYSFVEAINTLIDPAYLRGPFKQVAVAVADAPPAPFTQAAYHL 120
DB 322 VRKPLDFESQRSYSFVEAINTLIDPAYLRGPFKQVAVAVADAPPAPFTQAAYHL 381

QY 121 TYPENKAPGTLVGOISADLDPSPAPIRYSILPHSDPERCPSIOPEGTHTTAAPLDREA 180
DB 382 TYPENKAPGTLVGOISADLDPSPAPIRYSILPHSDPERCPSIOPEGTHTTAAPLDREA 441
QY 181 RAMNLT/LATEL 193
DB 442 RAMNLT/LATEL 454

RESULT 10
ABR40114
ID ABR40114 standard; protein; 781 AA.
XX ABR40114;
AC ABR40114;
DT 04-JUL-2003 (first entry)
XX

Human cell adhesion and extracellular matrix protein, CADECM-11.
XX
XX Human; anti-HIV; antiallergic; cerebroprotective; antiParkinsonian;
XX anticonvulsant; nootropic; neuroprotective; immunosuppressive;
XX dermatological; anti-inflammatory; cytostatic; antiatherosclerotic;
XX gene therapy; cell adhesion; extracellular matrix; CADECM;
XX immune system disorder; AIDS; allergy; neurological disorder; stroke;
XX Parkinson's disease; epilepsy; developmental disorder; Down's syndrome;
XX cerebral palsy; connective tissue disorder; systemic lupus erythematosus;
XX genetic disorder; Alport's syndrome; cell proliferative disorder; cancer;
XX atherosclerosis.

XX Homo sapiens.
XX
XX WO2003027230-A2.
XX
XX 03-APR-2003.
XX
XX 02-AUG-2002; 2002WO-US024649.
XX
XX 03-AUG-2001; 2001US-0309964P.
XX 17-AUG-2001; 2001US-0310139P.
XX 31-AUG-2001; 2001US-0316771P.
XX 07-SEP-2001; 2001US-0317896P.
XX 21-SEP-2001; 2001US-0324781P.
XX 05-OCT-2001; 2001US-0327606P.
XX 12-OCT-2001; 2001US-0328960P.
XX 09-NOV-2001; 2001US-0344471P.
XX 17-MAY-2002; 2002US-0381291P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Burford N, Warren BA, Duggan BM, Mason PM, Richardson TW, Yue H;
XX Forsythe J, Elliott VS, Griffith JA, Gervad AE, Azimzai Y,
XX Kalliock DA, Xu Y, Honchel CD, Baughn MR, Gietzen KJ, Lee S,
XX Wala NK, Tang YT, Nguyen DB, Becha SD, Lee SY, Ramkumar J;
XX WPI; 2003-354645/33.
XX N-PSDB; ACC00402.
XX
XX New human cell adhesion and extracellular matrix proteins (CADECM),
XX useful for diagnosing, treating or preventing disorders associated with
XX aberrant CADECM expression, e.g. cancer, AIDS, atherosclerosis, allergies
XX or stroke.
XX
XX Claim 1; Page 192-194; 234pp; English.

XX The present invention relates to novel human cell adhesion and
XX extracellular matrix proteins, CADECM-1 to CADECM-22, and their coding
XX sequences (ACC00392-ACC00413 and ABR40104-ABR40125). The coding sequences
XX and proteins are useful in diagnosing, treating and preventing disorders
XX associated with aberrant expression of CADECM, such as immune system
XX disorders (e.g. AIDS or allergies), neurological disorders (e.g. stroke,
XX Parkinson's disease or epilepsy), developmental disorders (e.g. Down's

CC syndrome or cerebral palsy); connective tissue disorders (e.g. systemic
CC lupus erythematosus), genetic disorders (e.g. Alport's syndrome) or cell
CC proliferative disorders (e.g. cancer or atherosclerosis)
XX
XX Sequence 781 AA:
SQ
Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-100; Mismatches 0; Gaps 0;
Matches 193; Conservative 0; Indels 0;

QY 1 SLYQFSVETAGPGLVGRRAQDPDLDGNALMAYSLIDGSGAFSISDLOQRDGLT 60
DB 262 SLYQFSVETAGPGLVGRRAQDPDLDGNALMAYSLIDGSGAFSISDLOQRDGLT 321
QY 61 VKKPLDFESQSRYSFRVATNTLIDPAYLRGPFKDVASVVAQDAPPEPAFTQAAYHL 120
DB 322 VKKPLDFESQSRYSFRVATNTLIDPAYLRGPFKDVASVVAQDAPPEPAFTQAAYHL 381
QY 121 TYPENKAPGTLVGOISADLDPSPAPIRYSILPHSDPERCPSIOPEGTHTTAAPLDREA 180
DB 382 TYPENKAPGTLVGOISADLDPSPAPIRYSILPHSDPERCPSIOPEGTHTTAAPLDREA 441
QY 181 RAMNLT/LATEL 193
DB 442 RAMNLT/LATEL 454

RESULT 11
ADA01366
ID ADA01366 standard; protein; 781 AA.
XX
XX ADA01366;
AC ADA01366;
DT 06-NOV-2003 (first entry)
XX
XX Human PRO polypeptide #49.
XX
XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

XX Homo sapiens.
XX
XX US2003068779-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0290589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GENTECH) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
XX Gunney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2003-625484/59.
XX N-PSDB; ADA01365.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX Claim 11; Fig 98; 307pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and

transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO factor-alpha (TGF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for inducing endothelial cell tube formation and for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence represents a human PRO polypeptide of the invention.

Sequence 781 AA:

Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-100;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPTLVGRRAQDPDLGNALMAVSIIDGSESEAFSISTDLQGRDGLT 60
Db 262 SLVQFSVETAGPTLVGRRAQDPDLGNALMAVSIIDGSESEAFSISTDLQGRDGLT 321
QY 61 VRKLPDSESGRSYFRVEATNTLLDPAYLRGPFRVDVAVRVAQDAPEPPAFQAAYHL 120
Db 322 VRKLPDSESGRSYFRVEATNTLLDPAYLRGPFRVDVAVRVAQDAPEPPAFQAAYHL 381
QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 180
Db 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441
QY 181 RAWNLTIVLATEL 193
Db 442 RAWNLTIVLATEL 454

RESULT 12

ADA43795
ID ADA43795 standard; protein; 781 AA.

XX ADA43795;
XX AC
XX 20-NOV-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
XX endothelial cell tube formation; chondrocyte cell differentiation;
XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX liver tumour; cystostatic; vaccine.

XX Homo sapiens.

XX US2003064474-A1.

XX 03-APR-2003.

XX 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US0270399.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
XX WPI; 2003-605867/57.
XX N-PSDB; ADA43794.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
XX PRO21383, useful in molecular biology, chromosome and gene mapping, in
XX generating antisense RNA and DNA, and in gene therapy.

PS Claim 11; Fig 98; 308pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)
XX polypeptide, having at least 80% sequence identity to a sequence selected
XX from any one of the 57 amino acid sequences given in specification, or to
XX a sequence encoded by a nucleic acid molecule selected from any one of
XX the nucleic acids deposited under any of the ATCC accession numbers given
XX in specification, or a sequence having at least 80% identity to PRO
XX lacking its associated signal peptide, an extracellular domain of PRO
XX with or without its associated signal peptide. Also included are vectors,
XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
XX PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX an oligonucleotide probe derived from any one of the above nucleotide
XX sequences. PRO6018 polypeptide is useful for stimulating the
XX proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
XX and PRO21383 polypeptides are useful for stimulating the proliferation of
XX human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
XX polypeptides are useful for inhibiting the proliferation of human
XX microvascular endothelial cells. PRO polypeptides are useful for
XX detecting the presence of tumour in a mammal, including tumours of lung,
XX colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
XX PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO20933 and
XX PRO34274 polypeptides are useful for inducing endothelial cell tube
XX formation. PRO or the antibody are useful in the preparation of a
XX medicament for treating a condition responsive to PRO polypeptide. The
XX oligonucleotide probes are useful for isolating genomic and cDNA
XX nucleotide sequences, for measuring or detecting the expression of an
XX associated gene, and as antisense probes. PRO nucleic acid is useful as a
XX hybridisation probe, in chromosome and gene mapping, in the generation of
XX antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
XX PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence represents a PRO protein.

Sequence 781 AA:

Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5.6e-100;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPTLVGRRAQDPDLGNALMAVSIIDGSESEAFSISTDLQGRDGLT 60
Db 262 SLVQFSVETAGPTLVGRRAQDPDLGNALMAVSIIDGSESEAFSISTDLQGRDGLT 321
QY 61 VRKLPDSESGRSYFRVEATNTLLDPAYLRGPFRVDVAVRVAQDAPEPPAFQAAYHL 120
Db 322 VRKLPDSESGRSYFRVEATNTLLDPAYLRGPFRVDVAVRVAQDAPEPPAFQAAYHL 381
QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 180
Db 382 TVPENKAPGTLVGOISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441
QY 181 RAWNLTIVLATEL 193
Db 442 RAWNLTIVLATEL 454

RESULT 13

ADA43563
ID ADA43563 standard; protein; 781 AA.

XX

ADA43563;
20-NOV-2003 (first entry)
Human secreted/transmembrane polypeptide PRO34009.
Human, PRO; secreted protein; transmembrane protein;
endothelial cell tube formation; chondrocyte cell differentiation;
microvascular endothelial cell; tumour; lung tumour; colon tumour;
breast tumour; prostate tumour; rectal tumour; kidney tumour;
liver tumour; cytostatic; vaccine.
Homo sapiens.
US2003073196-A1.
17-APR-2003.
18-SEP-2002; 2002US-00246210.
04-APR-2001; 2001US-0282199P.
29-AUG-2001; 2001WO-US027099.
18-JUL-2002; 2002US-00197942.
(GETH) GENENTECH INC.
Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
Fong S;
WPI; 2003-743814/70.
N-PSDB; ADA43562.
New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PRO2183 useful for stimulating the proliferation or differentiation of
chondrocyte cells and detecting the presence of a tumor in a mammal.
Claim 11; Fig 98; 307pp; English.
The invention relates to an isolated secreted/transmembrane (PRO)
polypeptide, having at least 80% sequence identity to a sequence selected
from any one of the 57 amino acid sequences given in specification, or to
a sequence encoded by a nucleic acid molecule selected from any one of
the nucleic acids deposited under any of the ATCC accession numbers given
in specification, or a sequence having at least 80% identity to PRO
lacking its associated signal peptide, an extracellular domain of PRO
with or without its associated signal peptide. Also included are vectors,
PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
administering PRO281, PRO1560, PRO189, PRO4493, PRO6308, PRO6000,
PRO10275, PRO2107, PRO20933 or PRO34274 polypeptide or its agonist) and
an oligonucleotide probe derived from any one of the above nucleotide
sequences. PRO6018 polypeptide is useful for stimulating the
proliferation or differentiation of chondrocyte cells. PRO133, PRO20080
and PRO2183 polypeptides are useful for stimulating the proliferation of
human microvascular endothelial cells. PRO6071, PRO487 and PRO6006
polypeptides are useful for inhibiting the proliferation of human
microvascular endothelial cells. PRO polypeptides are useful for
detecting the presence of tumour in a mammal, including tumours of lung,
colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560
PRO189, PRO4493, PRO6308, PRO6000, PRO10275, PRO2127, PRO20933 and
PRO34274 polypeptides are useful for inducing endothelial cell tube
formation. PRO or the antibody are useful in the preparation of a
medicament for treating a condition responsive to PRO polypeptide. The
oligonucleotide probes are useful for isolating genomic and cDNA
nucleotide sequences, for measuring or detecting the expression of an
associated gene, and as antisense probes. PRO nucleic acid is useful as a
hybridisation probe, in chromosome and gene mapping, in the generation of
antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
present sequence represents a PRO protein.

Query Match 100.0%; Score 990; DB 6; Length 781;
Best Local Similarity 100.0%; Pred. No. 5,6e-100;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLVPSVETAGPGTLVLRRAQDPDGDNALMAYSLIDGSGAFSISDLOQRDGLT 60
DB 262 SLVPSVETAGPGTLVLRRAQDPDGDNALMAYSLIDGSGAFSISDLOQRDGLT 321
QY 61 VRKPLDFESQGSYSFRVATNTLIDPAYLRGPFKDVASVAVAQDAPPEPPAFOAAVHL 120
DB 322 VRKPLDFESQGSYSFRVATNTLIDPAYLRGPFKDVASVAVAQDAPPEPPAFOAAVHL 381
QY 121 TYPENKAPGTLVGOISAADLDPASPIRYSILPHSDPERCFISQPEEGTHTAAPLDREA 180
DB 382 TYPENKAPGTLVGOISAADLDPASPIRYSILPHSDPERCFISQPEEGTHTAAPLDREA 441
QY 181 RAMNHLTVLATEL 193
DB 442 RAMNHLTVLATEL 454
RESULT 14
ADA01238
ID ADA01238 standard; protein; 781 AA.
XX
AC ADA01238;
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human PRO polypeptide #49.
DE
XX
KW Human, PRO; secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor-alpha; TNF-alpha blood; chondrocyte cell; tumour;
cancer; lung; colon; breast; prostate; rectum; kidney; liver;
microvascular endothelial cell; endothelial cell tube formation.
XX
OS Homo sapiens.
XX
XX US2003068782-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245851.
XX
XX 27-APR-1999; 99US-0131271P.
XX 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
XX (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
DR WPI; 2003-625487/59.
DR N-PSDB; ADA01237.
XX
PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Claim 11; Fig 98; 308pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,

CC prostate, rectal, kidney and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for stimulating and inhibiting proliferation of human
 CC microvascular endothelial cells and for inducing endothelial cell tube
 CC formation. This sequence represents a human PRO polypeptide of the
 CC invention.

SO Sequence 781 AA:

Query Match 100.0%; Score 990; DB 6; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.6e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDGEGSEAFSISTDLOGRDGLLT 60
 DB 262 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDGEGSEAFSISTDLOGRDGLLT 321
 QY 61 VRKPLDFESQRSYSFRVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFTQAAYHL 120
 DB 322 VRKPLDFESQRSYSFRVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFTQAAYHL 381
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSLPHSDPERCFSTIOPEEGTHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSLPHSDPERCFSTIOPEEGTHTAAPLDREA 441
 QY 181 RAWENLTVLATEL 193
 DB 442 RAWENLTVLATEL 454

RESULT 15

ADA01122
 ID ADA01122 standard; protein; 781 AA.

ADA01122;

DT 06-NOV-2003 (first entry)

DE Human secreted/transmembrane polypeptide PRO34009.

XX Human; PRO; secreted protein; transmembrane protein;
 KW endothelial cell tube formation; chondrocyte cell differentiation;
 KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
 KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
 KW liver tumour; cytostatic; vaccine.

XX Homo sapiens.

XX US2003068780-A1.

XX 10-APR-2003.

XX 16-SEP-2002; 2002US-00245143.

XX 02-AUG-2000; 2000US-0222635P.

XX 20-JUN-2001; 2001WO-US019692.

XX 29-AUG-2001; 2001WO-US027039.

XX 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

XX Baker KP, Batton DL, Filvaroff E, Goddard A, Grimaldi JC,
 PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z,
 PI Fong S,
 XX WPI; 2003-625485/59.

DR N-PSDB; ADA01121.

XX Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 11; Fig 98; 307pp; English.

XX The invention relates to an isolated secreted/transmembrane (PRO)
 CC polypeptide, having at least 80% sequence identity to a sequence selected
 CC from any one of the 57 amino acid sequences given in specification, or to
 CC a sequence encoded by a nucleic acid molecule selected from any one of
 CC the nucleic acids deposited under any of the ATCC accession numbers given
 CC in specification, or a sequence having at least 80% identity to PRO
 CC lacking its associated signal peptide, an extracellular domain of PRO
 CC with or without its associated signal peptide. Also included are vectors,
 CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 CC administering PRO281, PRO1560, PRO449, PRO6308, PRO6000,
 CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
 CC an oligonucleotide probe derived from any one of the above nucleotide
 CC sequences. PRO6018 polypeptide is useful for stimulating the
 CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
 CC and PRO21383 polypeptides are useful for stimulating the proliferation of
 CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
 CC polypeptides are useful for inhibiting the proliferation of human
 CC microvascular endothelial cells. PRO polypeptides are useful for
 CC detecting the presence of tumour in a mammal, including tumours of lung,
 CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
 CC PRO189, PRO449, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
 CC PRO34274 polypeptides are useful for inducing endothelial cell tube
 CC formation. PRO or the antibody are useful in the preparation of a
 CC medicament for treating a condition responsive to PRO polypeptide. The
 CC oligonucleotide probes are useful for isolating genomic and cDNA
 CC nucleotide sequences, for measuring or detecting the expression of an
 CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
 CC hybridisation probe, in chromosome and gene mapping, in the generation of
 CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
 CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
 CC present sequence represents a PRO protein.

SO Sequence 781 AA:

Query Match 100.0%; Score 990; DB 7; Length 781;
 Best Local Similarity 100.0%; Pred. No. 5.6e-100;
 Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDGEGSEAFSISTDLOGRDGLLT 60
 DB 262 SLVQFSVETAGPGLVGRRLAQPDPDGNALMAYSLIDGEGSEAFSISTDLOGRDGLLT 321
 QY 61 VRKPLDFESQRSYSFRVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFTQAAYHL 120
 DB 322 VRKPLDFESQRSYSFRVEATNTLIDPAYLRGPFKDVASVRAVQDAPEPPAFTQAAYHL 381
 QY 121 TVPENKAPGTLVGOISADLDSPASPIRYSLPHSDPERCFSTIOPEEGTHTAAPLDREA 180
 DB 382 TVPENKAPGTLVGOISADLDSPASPIRYSLPHSDPERCFSTIOPEEGTHTAAPLDREA 441
 QY 181 RAWENLTVLATEL 193
 DB 442 RAWENLTVLATEL 454

Search completed: December 8, 2004, 10:13:07
 Job time : 80.866 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 8, 2004, 10:13:18 ; Search time 197.215 Seconds
(without alignments)
349.544 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVQFSVETAGPGLVGRLL.....APLDREARAHNITVLTATL 193

Scoring table: BLASTJ62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_AA*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	990	100.0	193	US-09-788-051-15
2	990	100.0	493	US-10-072-012-482
3	990	100.0	607	US-10-258-951-74
4	990	100.0	620	US-09-788-051-7
5	990	100.0	636	US-09-788-051-4
6	990	100.0	781	US-09-860-868-2
7	990	100.0	781	US-10-245-752-98
8	990	100.0	781	US-10-245-859-98
9	990	100.0	781	US-10-245-103-98
10	990	100.0	781	US-10-245-107-98
11	990	100.0	781	US-10-245-143-98
12	990	100.0	781	US-10-245-771-98
13	990	100.0	781	US-10-245-851-98

14	990	100.0	781	US-10-245-883-98	Sequence 98, Appl
15	990	100.0	781	US-10-237-535-98	Sequence 98, Appl
16	990	100.0	781	US-10-238-183-98	Sequence 98, Appl
17	990	100.0	781	US-10-238-283-98	Sequence 98, Appl
18	990	100.0	781	US-10-238-370-98	Sequence 98, Appl
19	990	100.0	781	US-10-245-055-98	Sequence 98, Appl
20	990	100.0	781	US-10-245-147-98	Sequence 98, Appl
21	990	100.0	781	US-10-245-730-98	Sequence 98, Appl
22	990	100.0	781	US-10-245-739-98	Sequence 98, Appl
23	990	100.0	781	US-10-246-210-98	Sequence 98, Appl
24	990	100.0	781	US-10-239-196-98	Sequence 98, Appl
25	990	100.0	781	US-10-243-024-98	Sequence 98, Appl
26	990	100.0	781	US-10-243-409-98	Sequence 98, Appl
27	990	100.0	781	US-10-245-621-98	Sequence 98, Appl
28	990	100.0	781	US-10-245-860-98	Sequence 98, Appl
29	990	100.0	781	US-10-245-033-98	Sequence 98, Appl
30	990	100.0	781	US-10-243-095-98	Sequence 98, Appl
31	990	100.0	781	US-10-245-185-98	Sequence 98, Appl
32	990	100.0	781	US-10-245-447-98	Sequence 98, Appl
33	990	100.0	781	US-10-245-473-98	Sequence 98, Appl
34	990	100.0	781	US-10-245-770-98	Sequence 98, Appl
35	990	100.0	781	US-10-245-877-98	Sequence 98, Appl
36	990	100.0	781	US-10-246-976-98	Sequence 98, Appl
37	990	100.0	781	US-10-243-320-98	Sequence 98, Appl
38	990	100.0	781	US-10-162-435-13	Sequence 13, Appl
39	990	100.0	781	US-10-242-743-98	Sequence 98, Appl
40	990	100.0	781	US-10-242-845-98	Sequence 98, Appl
41	990	100.0	781	US-10-238-325-98	Sequence 98, Appl
42	990	100.0	781	US-10-238-346-98	Sequence 98, Appl
43	990	100.0	781	US-10-238-411-98	Sequence 98, Appl
44	990	100.0	781	US-10-243-124-98	Sequence 98, Appl
45	990	100.0	781	US-10-243-124-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-09-788-051-15
Sequence 15, Application US/09788051
Publication No. US20030144491A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
APPLICANT: Kuo, Chiayun
APPLICANT: Arterburn, Matthew C
APPLICANT: Yeung, George
APPLICANT: Palencia, Servando
APPLICANT: Tang, Y Tom
APPLICANT: Lau, Chenghua
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES
FILE REFERENCE: HYS-39
CURRENT APPLICATION NUMBER: US/09/788,051
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/496,914
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
US-09-788-051-15

Query Match 100.0%; Score 990; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 2,2e+89;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SLVQFSVETAGPGLVGRLLRAQDPDLGNALMAYSLDGGSEAFSISTDLOGRDLT 60
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Db 1 SLVQFSVETAGPGLTVGRRAQDPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPKDVASVRVAVQDAPEPPAFQAAAYHL 120
Db 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPKDVASVRVAVQDAPEPPAFQAAAYHL 120
QY 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEGCTHTAAPLDREA 180
Db 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEGCTHTAAPLDREA 180
QY 181 RAMENLTVLATEL 193
Db 181 RAMENLTVLATEL 193

RESULT 2

US-10-072-482
/ Sequence 482, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zethusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangoli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taulier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grosse, William M.
/ APPLICANT: Alsebrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieser, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 482
/ LENGTH: 493
/ TYPE: PRT

/ ORGANISM: Homo sapiens
US-10-072-012-482
Query Match 100.0%; Score 990; DB 15; Length 493;
Best Local Similarity 100.0%; Pred. No. 7, 9e-89;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLVQFSVETAGPGLTVGRRAQDPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
Db 262 SLVQFSVETAGPGLTVGRRAQDPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPKDVASVRVAVQDAPEPPAFQAAAYHL 120
Db 322 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPKDVASVRVAVQDAPEPPAFQAAAYHL 381
QY 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEGCTHTAAPLDREA 180
Db 382 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEGCTHTAAPLDREA 441
QY 181 RAMENLTVLATEL 193
Db 442 RAMENLTVLATEL 454

RESULT 3

US-10-258-951-74
/ Sequence 74, Application US/10258951
/ Publication No. US2004003504A1
/ GENERAL INFORMATION:
/ APPLICANT: Mardock, Paul R.
/ APPLICANT: Rizvi, Safia K.
/ APPLICANT: Smith, Zhacail F.
/ APPLICANT: Xiang, Zhacail F.
/ APPLICANT: Kabnick, Karen
/ APPLICANT: Lai, Ying-Ta
/ APPLICANT: Xie, Qing
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GRS0025
/ CURRENT APPLICATION NUMBER: US/10/258,951
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: PCT/US01/13360
/ PRIOR FILING DATE: 2001-04-26
/ PRIOR APPLICATION NUMBER: 60/199,963
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 60/203,336
/ PRIOR FILING DATE: 2000-05-11
/ PRIOR APPLICATION NUMBER: 60/207,087
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/207,546
/ PRIOR FILING DATE: 2000-05-26
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for windows Version 3.0
/ SEQ ID NO 74
/ LENGTH: 607
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-258-951-74
Query Match 100.0%; Score 990; DB 15; Length 607;
Best Local Similarity 100.0%; Pred. No. 1e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLVQFSVETAGPGLTVGRRAQDPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
Db 262 SLVQFSVETAGPGLTVGRRAQDPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLT 321
QY 61 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPKDVASVRVAVQDAPEPPAFQAAAYHL 120
Db 322 VRKPLDFESQSRYSFRVEATNTLLIDPAYLRGPKDVASVRVAVQDAPEPPAFQAAAYHL 381
QY 121 TVPENKAPGLTVGOISADLDSPASPIRYSILPHSDPERCFSTIOPEGCTHTAAPLDREA 180

Db 382 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
Db 442 RAMHNLTVLATEL 454

RESULT 4

US-09-788-051-7
; Sequence 7, Application US/09788051
; Publication No. US2003014491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimnac, Radcoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-7

Query Match 100.0%; Score 990; DB 10; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLTVGRRAODPDLDGNALMAYSILDGSGSAFSTIDLOGRDGLT 60
Db 246 SLVQSVVETAGPGLTVGRRAODPDLDGNALMAYSILDGSGSAFSTIDLOGRDGLT 305
QY 61 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 120
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QY 121 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 366 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 425
QY 181 RAMHNLTVLATEL 193
Db 426 RAMHNLTVLATEL 438

RESULT 5

US-09-788-051-4
; Sequence 4, Application US/09788051
; Publication No. US2003014491A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada D
; APPLICANT: Kuo, Chiaoyun
; APPLICANT: Atterburn, Matthew C
; APPLICANT: Yeung, George
; APPLICANT: Palencia, Servando
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dimnac, Radcoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CADHERIN-LIKE POLYPEPTIDES AN
; FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

FILE REFERENCE: HYS-39
; CURRENT APPLICATION NUMBER: US/09/788,051
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-051-4

Query Match 100.0%; Score 990; DB 10; Length 636;
Best Local Similarity 100.0%; Pred. No. 1.1e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLTVGRRAODPDLDGNALMAYSILDGSGSAFSTIDLOGRDGLT 60
Db 262 SLVQSVVETAGPGLTVGRRAODPDLDGNALMAYSILDGSGSAFSTIDLOGRDGLT 321
QY 61 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 120
Db 322 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 382 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
Db 442 RAMHNLTVLATEL 454

RESULT 6

US-09-860-868-2
; Sequence 2, Application US/09860868
; Patent No. US20020076757A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, ROY A.J.
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-050001
; CURRENT APPLICATION NUMBER: US/09/860,868
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,674
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-868-2

Query Match 100.0%; Score 990; DB 9; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLTVGRRAODPDLDGNALMAYSILDGSGSAFSTIDLOGRDGLT 60
Db 262 SLVQSVVETAGPGLTVGRRAODPDLDGNALMAYSILDGSGSAFSTIDLOGRDGLT 321
QY 61 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 120
Db 322 VRKPLDFESQRSYFRVEATNTLIDPAYLRGPFKDVA SVRAVQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 180
Db 382 TVPENKAGTIVGQISADLDSPASPIRYSILPHSDPERCFSTIOPEEGTHTAAPLDREA 441


```
RESULT 9
US-10-245-103-98
; Sequence 98, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bacon, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-103-98

Query Match      100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 60
DB 262 SLVQSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 321
QY 61 VRKPLDFESQRSYFRVATNTLIDPAYLRGPFQDVASVRAVQDAPEPPAFTQAAYHL 120
DB 322 VRKPLDFESQRSYFRVATNTLIDPAYLRGPFQDVASVRAVQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGITHAAPLDREA 180
DB 382 TVPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGITHAAPLDREA 441
QY 181 RAWHNLTVLATEL 193
DB 442 RAWHNLTVLATEL 454

RESULT 10
```

```
US-10-245-107-98
; Sequence 98, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Bacon, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watande, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-98

Query Match      100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 60
DB 262 SLVQSVETAGPGLVGRRAQDPDLGDNALMAYSIIDGESSEAFSISTDQGRDGLT 321
QY 61 VRKPLDFESQRSYFRVATNTLIDPAYLRGPFQDVASVRAVQDAPEPPAFTQAAYHL 120
DB 322 VRKPLDFESQRSYFRVATNTLIDPAYLRGPFQDVASVRAVQDAPEPPAFTQAAYHL 381
QY 121 TVPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGITHAAPLDREA 180
DB 382 TVPENKAGTLVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGITHAAPLDREA 441
QY 181 RAWHNLTVLATEL 193
DB 442 RAWHNLTVLATEL 454

RESULT 11
US-10-245-143-98
; Sequence 98, Application US/10245143
```

```
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Matanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-143-98

Query Match      100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVGFSVVETAGPGTLVGRRAODPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVGFSVVETAGPGTLVGRRAODPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLLT 321
QY 61 VRKPLDFESQSYSFREYEAATNTLLDPAYLRGPKDVASVRVAQDAPEPPAFYQAAYHL 120
DB 322 VRKPLDFESQSYSFREYEAATNTLLDPAYLRGPKDVASVRVAQDAPEPPAFYQAAYHL 381
QY 121 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 382 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 441
QY 181 RAMNHLTVLATEL 193
DB 442 RAMNHLTVLATEL 454

RESULT 12
US-10-245-771-98
; Sequence 98, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
```

```
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Matanbe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-98

Query Match      100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVGFSVVETAGPGTLVGRRAODPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVGFSVVETAGPGTLVGRRAODPDLDGNALMAYSLIDEGSEAFSISTDLQGRDGLLT 321
QY 61 VRKPLDFESQSYSFREYEAATNTLLDPAYLRGPKDVASVRVAQDAPEPPAFYQAAYHL 120
DB 322 VRKPLDFESQSYSFREYEAATNTLLDPAYLRGPKDVASVRVAQDAPEPPAFYQAAYHL 381
QY 121 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 382 TVPENKAPGTLVGOISAADLSPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 441
QY 181 RAMNHLTVLATEL 193
DB 442 RAMNHLTVLATEL 454

RESULT 13
US-10-245-851-98
; Sequence 98, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO: 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-851-98

Query Match      100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGEGSEAFSISTDLQGRDGLLT 321
QY 61 VRKPLDFESQRSYSFVEATNTLIDPAYLRGPFKDVASVAVQDAPPPAFTQAAYHL 120
DB 322 VRKPLDFESQRSYSFVEATNTLIDPAYLRGPFKDVASVAVQDAPPPAFTQAAYHL 381
QY 121 TVPENKAPGLTVGQISAADLDSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREA 180
DB 382 TVPENKAPGLTVGQISAADLDSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
DB 442 RAMHNLTVLATEL 454
```

```

RESULT 14
US-10-245-883-98
; Sequence 98, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
```

```

; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C70
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-10-24
; PRIOR FILING DATE: 1997-11-10
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-05-22
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-02
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-18
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO: 98
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-883-98

Query Match      100.0%; Score 990; DB 14; Length 781;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 1 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGEGSEAFSISTDLQGRDGLLT 60
DB 262 SLVQFSVETAGPGLTVGRRAQDDPLGDNALMAYSILDGEGSEAFSISTDLQGRDGLLT 321
QY 61 VRKPLDFESQRSYSFVEATNTLIDPAYLRGPFKDVASVAVQDAPPPAFTQAAYHL 120
DB 322 VRKPLDFESQRSYSFVEATNTLIDPAYLRGPFKDVASVAVQDAPPPAFTQAAYHL 381
QY 121 TVPENKAPGLTVGQISAADLDSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREA 180
DB 382 TVPENKAPGLTVGQISAADLDSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREA 441
QY 181 RAMHNLTVLATEL 193
DB 442 RAMHNLTVLATEL 454
```

```

RESULT 15
US-10-237-535-98
; Sequence 98, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
```

APPLICANT: Smith,Victoria
APPLICANT: Stephan,Jean-Phillippe
APPLICANT: Matande,Colin
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
APPLICANT: Fong,Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R13
CURRENT FILING DATE: US/10/237,535
PRIOR APPLICATION NUMBER: 2002-09-06
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089601
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/106932
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119342
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/133957
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123972
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/127372
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/131271
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/133459
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/135725
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135729
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/135750
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138385
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/140653
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144732
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/144790
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/15228
PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146843
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/148188
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/148513
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/149327
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149395
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/150114
PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/151700
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151734
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/177118
PRIOR FILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: 60/179851
PRIOR FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 60/180921
PRIOR FILING DATE: 2000-02-06
PRIOR APPLICATION NUMBER: 60/187202
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/198587
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 60/199614
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/206330
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206368
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/209832
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 60/218371
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/222695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/22896
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230621
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/232887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/235147
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/261878
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/261910
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/261939
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/262150
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/26395
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/266421
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/267623
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/274399
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/280982
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/282129

PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/282199
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/290589
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 09/180997
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: 09/267213
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/403297
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 09/423741
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 09/709238
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 09/802706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/927796
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/929404
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/931836
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 10/001054
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 10/091056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 10/119480
PRIOR FILING DATE: 2002-04-09

Query Match 100.0%; Score 990; DB 14; Length 781;

Best Local Similarity 100.0%; Pred. No. 1.5e-88; Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAODPDLDGNALMAYSIIDGEGSEAFSISTDLQGRDGLT 60
DB 262 SLVQFSVETAGPGLVGRRAODPDLDGNALMAYSIIDGEGSEAFSISTDLQGRDGLT 321
QY 61 VRKPLDFESSORSYSRRVATNTLLIDPAYLRGPFKDVASVRVAODAPEPAFTQAAVHL 120
DB 322 VRKPLDFESSORSYSRRVATNTLLIDPAYLRGPFKDVASVRVAODAPEPAFTQAAVHL 381
QY 121 TVPENKAPGLTVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 180
DB 382 TVPENKAPGLTVGQISADLDSPASPIRYSILPHSDPERCFSIQPEEGTHTAAPLDREA 441
QY 181 RAMENLTVLATEL 193
DB 442 RAMENLTVLATEL 454

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2004, 09:16:13 ; Search time 23.0142 Seconds
(without alignments)
556.152 Million cell updates/sec

Title: US-09-788-051-15

Perfect score: 990
Sequence: 1 SLVQFSVETAGPGTLVGR.....APLDREARAHNLTVALTEL 193

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCtus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	54.5	693	2	US-08-738-349-6
2	540	54.5	693	4	US-09-918-497-55
3	540	54.5	796	2	US-08-738-349-4
4	537	54.2	796	1	US-08-188-228-58
5	537	54.2	796	1	US-08-332-643-52
6	537	54.2	796	1	US-08-332-643-58
7	537	54.2	796	4	US-09-654-328-2
8	532	53.7	796	2	US-08-738-349-2
9	522	52.7	532	1	US-08-188-228-44
10	522	52.7	532	1	US-08-332-638-44
11	522	52.7	799	1	US-08-188-228-42
12	522	52.7	799	1	US-08-332-638-42
13	521	52.6	793	1	US-08-188-228-54
14	521	52.6	793	1	US-08-332-643-48
15	521	52.6	793	1	US-08-332-638-54
16	459	46.4	653	1	US-08-188-228-46
17	459	46.4	653	1	US-08-332-638-46
18	447	45.2	615	2	US-08-738-349-12
19	407	41.1	794	1	US-08-188-228-60
20	407	41.1	794	1	US-08-332-643-54
21	407	41.1	794	1	US-08-332-638-60
22	314.5	31.8	780	1	US-08-188-228-50
23	314.5	31.8	780	1	US-08-332-643-44
24	314.5	31.8	780	1	US-08-332-638-50
25	203	20.5	712	2	US-08-474-067-2
26	203	20.5	712	2	US-08-474-067-5
27	203	20.5	712	2	US-08-474-068A-2

28	203	20.5	712	2	US-08-474-068A-5	Sequence 5, Appli
29	203	20.5	712	2	US-08-472-481-2	Sequence 2, Appli
30	203	20.5	717	2	US-08-474-067-4	Sequence 4, Appli
31	203	20.5	717	2	US-08-474-068A-4	Sequence 4, Appli
32	203	20.5	717	2	US-08-472-481-4	Sequence 7, Appli
33	200	20.2	837	2	US-08-474-067-7	Sequence 7, Appli
34	200	20.2	837	2	US-08-474-068A-7	Sequence 6, Appli
35	200	20.2	837	2	US-08-472-481-6	Sequence 6, Appli
36	198.5	20.1	713	1	US-08-188-228-62	Sequence 56, Appli
37	198.5	20.1	713	1	US-08-332-638-56	Sequence 62, Appli
38	198.5	20.1	713	1	US-08-332-638-62	Sequence 95, Appli
39	198.5	20.1	1026	1	US-07-998-003A-95	Sequence 95, Appli
40	198.5	20.1	1026	1	US-08-453-274B-95	Sequence 95, Appli
41	198.5	20.1	1026	1	US-08-453-695A-95	Sequence 95, Appli
42	198.5	20.1	1026	1	US-08-268-161A-95	Sequence 95, Appli
43	198.5	20.1	1026	2	US-08-453-702A-95	Sequence 95, Appli
44	198.5	20.1	1026	3	US-09-099-639-95	Sequence 95, Appli
45	198.5	20.1	1026	5	PCT-US93-12588-95	Sequence 95, Appli

ALIGNMENTS

RESULT 1
US-08-738-349-6
Sequence 6, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sumao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shuji
APPLICANT: Teijimura, Atsushi
APPLICANT: Amano, Egon
TITLE OR INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OR INVENTION: Process for its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-6

Query Match 54.5%; Score 540; DB 2; Length 693;
Best Local Similarity 51.8%; Pred. No. 1,1e-53;
Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 1 SVYQISVSEAAVPEEVEGRVAKDPDGENGLVTYINIVDDGMESEFITTDTYTOEGVIX 60
DB 271 SVYQISVSEAAVPEEVEGRVAKDPDGENGLVTYINIVDDGMESEFITTDTYTOEGVIX 330
QY VRKPLDPESQSYSFVEATNTLLIDPAYLRGPFKDVASVAVQDAPBPAPFTQAAYHL 120
DB 331 LKKVDPETKRAVSLKVEANVHIDPKFISNGPFKDTVTKIAVEDADEPMPFLAPSYIH 390
QY 121 TVPENKAPGTLVGOISAADLDPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 391 EVQENMAAGTVGVGVHAKDPDANSPIRYSIDRHTDLDRFTINPEDGFKTKPLDREE 450
QY 181 RAMNLTVLATEL 193
DB 451 TAWLNTVFAAEI 463

RESULT 2

US-09-919-497-55
; Sequence 55, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutecr, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-55

Query Match 54.5%; Score 540; DB 4; Length 693;
Best Local Similarity 51.8%; Pred. No. 1,1e-53;
Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 1 SVYQISVSEAAVPEEVEGRVAKDPDGENGLVTYINIVDDGMESEFITTDTYTOEGVIX 60
DB 271 SVYQISVSEAAVPEEVEGRVAKDPDGENGLVTYINIVDDGMESEFITTDTYTOEGVIX 330
QY VRKPLDPESQSYSFVEATNTLLIDPAYLRGPFKDVASVAVQDAPBPAPFTQAAYHL 120
DB 331 LKKVDPETKRAVSLKVEANVHIDPKFISNGPFKDTVTKIAVEDADEPMPFLAPSYIH 390
QY 121 TVPENKAPGTLVGOISAADLDPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 391 EVQENMAAGTVGVGVHAKDPDANSPIRYSIDRHTDLDRFTINPEDGFKTKPLDREE 450
QY 181 RAMNLTVLATEL 193
DB 451 TAWLNTVFAAEI 463

RESULT 3
US-08-738-349-4
; Sequence 4, Application US/08738349
; Patent No. 5869638
; GENERAL INFORMATION:
; APPLICANT: Takeshita, Sunao
; APPLICANT: Okazaki, Makoto
; APPLICANT: Kawai, Shinji
; APPLICANT: Tsujimura, Akiyoshi
; APPLICANT: Amann, Egon
; TITLE OF INVENTION: Bone-Related Cadherin-like Protein and

TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-738-349-4

Query Match 54.5%; Score 540; DB 2; Length 796;
Best Local Similarity 51.8%; Pred. No. 1,1e-53;
Matches 100; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 1 SVYQISVSEAAVPEEVEGRVAKDPDGENGLVTYINIVDDGMESEFITTDTYTOEGVIX 60
DB 271 SVYQISVSEAAVPEEVEGRVAKDPDGENGLVTYINIVDDGMESEFITTDTYTOEGVIX 330
QY VRKPLDPESQSYSFVEATNTLLIDPAYLRGPFKDVASVAVQDAPBPAPFTQAAYHL 120
DB 331 LKKVDPETKRAVSLKVEANVHIDPKFISNGPFKDTVTKIAVEDADEPMPFLAPSYIH 390
QY 121 TVPENKAPGTLVGOISAADLDPASPIRYSILPHSDPERCFSTQPEEGTHTAAPLDREA 180
DB 391 EVQENMAAGTVGVGVHAKDPDANSPIRYSIDRHTDLDRFTINPEDGFKTKPLDREE 450
QY 181 RAMNLTVLATEL 193
DB 451 TAWLNTVFAAEI 463

RESULT 4
US-08-188-228-58
; Sequence 58, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-58

Query Match 54.2%; Score 537; DB 1; Length 796;
Best Local Similarity 51.6%; Pred. No. 3.1e-53;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQSVETAGPGLVGRIRADPDLDGNALMAYSLDGGSEAFSISTDLQGRGLTV 61
DB 272 LYQMSVSAAVGEEVGRVAKDPDIGNGLVTYNIVDGMESFEITTDYETGVIKL 331
QY 62 RKPLDFESQRSYFRVEATNTLIDPAYLRGPFQDVASVRVAVODAPPEPAFTQAAVHLT 121
DB 332 KKPVDFTERRAYSLKVEANVHIDPKFISNGPFKQTVKISVEDADEPPEFLAPSYIHE 391
QY 122 VPEKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFISIOPEEGTHTAAPLDREAR 181
DB 392 VQENAAAGTVGRVAKDPDANSPIRYSIDRHTDLDRFFITNPEDGFIKTKRLDREBT 451

QY 182 AMHNLTVLATEL 193
DB 452 AMNLTVPAAEI 463

RESULT 5
US-08-332-643-52
Sequence 52, Application US/08332643
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-52

Query Match 54.2%; Score 537; DB 1; Length 796;
Best Local Similarity 51.6%; Pred. No. 3.1e-53;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LYQSVETAGPGLVGRIRADPDLDGNALMAYSLDGGSEAFSISTDLQGRGLTV 61
DB 272 LYQMSVSAAVGEEVGRVAKDPDIGNGLVTYNIVDGMESFEITTDYETGVIKL 331
QY 62 RKPLDFESQRSYFRVEATNTLIDPAYLRGPFQDVASVRVAVODAPPEPAFTQAAVHLT 121
DB 332 KKPVDFTERRAYSLKVEANVHIDPKFISNGPFKQTVKISVEDADEPPEFLAPSYIHE 391
QY 122 VPEKAPGTLVGQISADLDSPASPIRYSILPHSDPERCFISIOPEEGTHTAAPLDREAR 181
DB 392 VQENAAAGTVGRVAKDPDANSPIRYSIDRHTDLDRFFITNPEDGFIKTKRLDREBT 451

QY 182 AMHNLTVLATEL 193
DB 452 AMNLTVPAAEI 463

RESULT 6
US-08-332-638-58
Sequence 58, Application US/08332638
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-58

Query Match

Best Local Similarity 54.2%; Score 537; DB 1; Length 796;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LVQSVVETAGPGLVGRRLAOPDGLDGNALMAVSLIDGEGSAFISITDLOGRDGLTV 61
DB 272 LVQMSVSEAAPGSEVGRVAKDPDIGNGLVTYNIIVDGGMSFELTTDYETQSGVTK 331
QY 62 RKPLDFESQSRYSFRVATNTLLDPAYLRGPFKCVASVAVQADAPPPAFQAAHYLT 121
DB 332 KKPVDFFETERYASLKVEAAVNHIDPKFISNGPFKDTVTVKISVEDADEPMPFLAPSYIHE 391
QY 122 VPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFISIOEEGTITTAFLDREAR 181
DB 392 VQENAAAGTVGRVHADPPDANSPIRYSIDRHTDLDREFTINPEDFIKTTKPLDREFT 451
QY 182 AMNLTVLATEL 193
DB 452 AMNLTVPAAEI 463

RESULT 7

US-09-654-328-2
Sequence 2, Application US/09654328
Patent No. 6787136
GENERAL INFORMATION:
APPLICANT: Brenner, Michael B.
TITLE OF INVENTION: Methods and Compositions for Treatment
FILE REFERENCE: B0801/7187/ERE/MAT
CURRENT APPLICATION NUMBER: US/09/654,328
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/152,456
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: US 60/153,490
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 796
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-654-328-2

Query Match

Best Local Similarity 54.2%; Score 537; DB 4; Length 796;
Matches 99; Conservative 41; Mismatches 52; Indels 0; Gaps 0;

QY 2 LVQSVVETAGPGLVGRRLAOPDGLDGNALMAVSLIDGEGSAFISITDLOGRDGLTV 61
DB 272 LVQMSVSEAAPGSEVGRVAKDPDIGNGLVTYNIIVDGGMSFELTTDYETQSGVTK 331

QY 62 RKPLDFESQSRYSFRVATNTLLDPAYLRGPFKCVASVAVQADAPPPAFQAAHYLT 121

DB 332 KKPVDFFETERYASLKVEAAVNHIDPKFISNGPFKDTVTVKISVEDADEPMPFLAPSYIHE 391

QY 122 VPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFISIOEEGTITTAFLDREAR 181

DB 392 VQENAAAGTVGRVHADPPDANSPIRYSIDRHTDLDREFTINPEDFIKTTKPLDREFT 451

QY 182 AMNLTVLATEL 193
DB 452 AMNLTVPAAEI 463

RESULT 8

US-08-738-349-2
Sequence 2, Application US/08738349
Patent No. 5869638
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Okazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Eggon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
FILING DATE:
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, W. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1233-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-738-349-2

Query Match

Best Local Similarity 53.7%; Score 532; DB 2; Length 796;
Matches 98; Conservative 42; Mismatches 53; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLVGRRLAOPDGLDGNALMAVSLIDGEGSAFISITDLOGRDGLTV 60
DB 271 SVQMSVSEAAPGSEVGRVAKDPDIGNGLVTYNIIVDGGMSFELTTDYETQSGVTK 330
QY 61 VRKPLDFESQSRYSFRVATNTLLDPAYLRGPFKCVASVAVQADAPPPAFQAAHYLT 120

Db 331 LKKVDEFTKRAYSLKLEAAVWHIDPFKISNGPFKDVTKISVEDADEPFWLAA5YH 390
Qy 121 TVPENKAPGLTVGQISADLDSPPASPIRYSILPHSDPERGCSLOPEGTHTAFLDREA 180
Db 391 EVQENAAAGTVGVGHAKDPDPAANSPIRYSIDRHTDLRPFITINPEDGFIKTKKPLDREB 450
Qy 181 RAMNLTVALTEL 193
Db 451 TAMLNISTVFAEI 463

RESULT 9
US-08-188-228-44
; Sequence 44, Application US/08188228
; Patent No. 5597725

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-188-228-44

Query Match 52.7%; Score 522; DB 1; Length 532;
Best Local Similarity 49.7%; Pred. No. 9.2e-52;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

Qy 1 SLVQFSVYETAGPGTLVGRLEAOPDLDGNALMAVSIIDGSGSAFSTIDLGSDGLT 60
Db 279 SLHRSVPEVDVVLGALGRVANDODIGENAOSSYDIIIDGTLFETISDAQADGVIR 338
Qy 61 VRKLPDESORSYSFRVEATNTLIDPAYLRGPFQDVASVRVAVQDAPEPPAFTQAAYHL 120
Db 339 LRKPLDFETKSKYTLKVEAANIHIIDPRFSGRPFQDTATVKIIVEDADEPVSPTYLL 398
Qy 121 TVPENKAPGLTVGQISADLDSPPASPIRYSILPHSDPERGCSLOPEGTHTAFLDREA 180

Db 399 EVHENAALNSVIGQYATARDPDITSSPIRFSIDRHTDLERQFNINADDKITLATELDEL 458
Qy 181 RAMNLTVALTEL 193
Db 459 SVWHNISTITATEI 471

RESULT 10
US-08-332-638-44
; Sequence 44, Application US/08332638
; Patent No. 5646250

GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-44

Query Match 52.7%; Score 522; DB 1; Length 532;
Best Local Similarity 49.7%; Pred. No. 9.2e-52;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

Qy 1 SLVQFSVYETAGPGTLVGRLEAOPDLDGNALMAVSIIDGSGSAFSTIDLGSDGLT 60
Db 279 SLHRSVPEVDVVLGALGRVANDODIGENAOSSYDIIIDGTLFETISDAQADGVIR 338
Qy 61 VRKLPDESORSYSFRVEATNTLIDPAYLRGPFQDVASVRVAVQDAPEPPAFTQAAYHL 120
Db 339 LRKPLDFETKSKYTLKVEAANIHIIDPRFSGRPFQDTATVKIIVEDADEPVSPTYLL 398
Qy 121 TVPENKAPGLTVGQISADLDSPPASPIRYSILPHSDPERGCSLOPEGTHTAFLDREA 180
Db 399 EVHENAALNSVIGQYATARDPDITSSPIRFSIDRHTDLERQFNINADDKITLATELDEL 458
Qy 181 RAMNLTVALTEL 193
Db 459 SVWHNISTITATEI 471

RESULT 11
US-08-188-228-42
; Sequence 42, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,228
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/049,460
; FILING DATE: 19 APR 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5597725and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-228-42

Query Match 52.7%; Score 522; DB 1; Length 799;
Best Local Similarity 49.7%; Pred. No. 1.7e-51;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLVGRRAOPDLGDNALMAYSLIDGEGSEAFSISTDLQGRDGLLT 60
DB 279 SLVHFSVPEDVLTGTAIGRVKANDQDIGNHOSYDIIDDDGTALFEITSDAQADQVIR 338
QY 61 VRKPLDEFSQSYSFREVEATNTLLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
DB 339 LRKPLDEFETKSYTLKVEANINHIDPFSGRGPFKDTATVKIYVEDADEPPVFSPTYLL 398
QY 121 TVPENKAPGLTVQGISADLDSPASPIRYSILPHSDPERCESIQPEEGTHTAAPLDREA 180
DB 399 EVHENALNSVIGQVATARDPDTITSSPIRFSIDRHTIDEROFINADDKITLATPLDREL 458
QY 181 RAWNLTVALTEL 193
DB 459 SVMNHSIATETI 471

RESULT 12
US-08-332-638-42
; Sequence 42, Application US/08332638
; Patent No. 5646250

; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,638
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,643
; FILING DATE: 17 APR 1992
; APPLICATION NUMBER: US/08/049,460
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646250and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-332-638-42

Query Match 52.7%; Score 522; DB 1; Length 799;
Best Local Similarity 49.7%; Pred. No. 1.7e-51;
Matches 96; Conservative 42; Mismatches 55; Indels 0; Gaps 0;

QY 1 SLVQSVVETAGPGLVGRRAOPDLGDNALMAYSLIDGEGSEAFSISTDLQGRDGLLT 60
DB 279 SLVHFSVPEDVLTGTAIGRVKANDQDIGNHOSYDIIDDDGTALFEITSDAQADQVIR 338
QY 61 VRKPLDEFSQSYSFREVEATNTLLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAYHL 120
DB 339 LRKPLDEFETKSYTLKVEANINHIDPFSGRGPFKDTATVKIYVEDADEPPVFSPTYLL 398
QY 121 TVPENKAPGLTVQGISADLDSPASPIRYSILPHSDPERCESIQPEEGTHTAAPLDREA 180
DB 399 EVHENALNSVIGQVATARDPDTITSSPIRFSIDRHTIDEROFINADDKITLATPLDREL 458
QY 181 RAWNLTVALTEL 193
DB 459 SVMNHSIATETI 471

RESULT 13
US-08-188-228-54
; Sequence 54, Application US/08188228
; Patent No. 5597725
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Shintaro
; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESS: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 559725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-189-228-54

Query Match 52.6%; Score 521; DB 1; Length 793;
Best Local Similarity 49.7%; Pred. No. 2.2e-51;
Matches 96; Conservative 41; Mismatches 56; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAQDDPLDGNALMAYSLIDGEGSEAFSISTDLQGRDGLT 60
DB 272 SLVHFSVPEDEVVLGTAIGRVKANDQDIGNAQSSYDIIDGGTALFEITSDAQADGIR 331
QY 61 VRKPLDFESQSSYSFRVATNTLIDPAYLRGPFKDVASVRVAVQDAPEPPFTQAAYHL 120
DB 332 LRKPLDFETKSYTLKDEANVHIDPRSGRPFKDTATVIVEDADEPVPVSSPTVLL 391
QY 121 TVPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFISIQEEGTHTAAPLDREA 180
DB 392 EVHENAALNSVIGVYARPDITSSPIRFSIDRHTDLERQFINADQKITLATPLDREL 451

QY 181 RAMHNLTVLATEL 193
DB 452 SVMHNTIITATEI 464

RESULT 14
US-08-332-643-48
Sequence 48, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 984-9740
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-643-48

Query Match 52.6%; Score 521; DB 1; Length 793;
Best Local Similarity 49.7%; Pred. No. 2.2e-51;
Matches 96; Conservative 41; Mismatches 56; Indels 0; Gaps 0;

QY 1 SLVQFSVETAGPGLVGRRAQDDPLDGNALMAYSLIDGEGSEAFSISTDLQGRDGLT 60
DB 272 SLVHFSVPEDEVVLGTAIGRVKANDQDIGNAQSSYDIIDGGTALFEITSDAQADGIR 331
QY 61 VRKPLDFESQSSYSFRVATNTLIDPAYLRGPFKDVASVRVAVQDAPEPPFTQAAYHL 120
DB 332 LRKPLDFETKSYTLKDEANVHIDPRSGRPFKDTATVIVEDADEPVPVSSPTVLL 391
QY 121 TVPENKAPGLVGOISADLDSPASPIRYSILPHSDPERCFISIQEEGTHTAAPLDREA 180
DB 392 EVHENAALNSVIGVYARPDITSSPIRFSIDRHTDLERQFINADQKITLATPLDREL 451

QY 181 RAMHNLTVLATEL 193
DB 452 SVMHNTIITATEI 464

RESULT 15
US-08-332-638-54
Sequence 54, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-638-54

Query Match 52.6%; Score 521; DB 1; Length 793;

Best Local Similarity 49.7%; Pred. No. 2.2e-51; Mismatches 56; Indels 0; Gaps 0;

Matches 96; Conservative 41; Mismatches 56; Indels 0; Gaps 0;

Qy 1 SLVQSVYETAGPGLVGRRAODPDLGDNALMAYSLIDEGSEAFSISTDLQGRDGLT 60
Db 272 SLVHFSYEDVYLGTAIGRVKANDQDIGNAQSSYDIIDGDTALFEITSDAQAGDIIR 331
Qy 61 VRKPLDPESSQSSYFRVEATNTLIDPAYLRGPFKDYASRVAVQDAPEPPAFTQAAYHL 120
Db 332 LRKPLDPEIKKSYTLKDEANVHIDPRFSGRGPPKDTATVIVEDADEPPVFSPTYLL 391
Qy 121 TVPENKAPGTLVQGISADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAPLDREA 180
Db 392 EVHENAALNSVIGVTAARDPDTSSPIRFSIDKHTDIERQFNINADDKITLALTPLDREL 451
Qy 181 RAWNLTVLATEL 193
Db 452 SVMNHTITLATEI 464

Search completed: December 8, 2004, 10:01:15
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